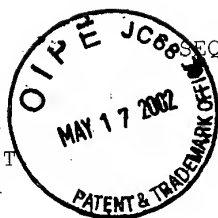


#24



## SEQUENCE LISTING

<110> Cali, Brian M.  
Holtzman, Doug  
Madden, Kevin T  
Milna, G. Todd  
Sherman, Amir  
Silva, Jeffry C.  
Trueheart, Josh  
Zhang, Lixin

<120> Novel Regulators of Fungal Gene Expression

<130> MIC-004

<140> US 10/029,180

<141> 2001-12-22

<150> US 60/257,431

<151> 2000-12-22

<160> 138

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 1

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cgcaccgacg atcctaactc ggtcaagctt ctcgagcgat acgaccagtg gtttgataac 180
aatggcttcg cgaagctgct gtctgctcgc atggcaagca aagaaaagtcg gaagaaaaga 240
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gagaccgagg gctccagcac tctgcaatg ccagccaccc ccaaccctga ttaccttgat 360
cctcgcttgg ccgattctca caatgacaac cagcaacatg cgggtacaac cctcgcagca 420
agcatcccaa accagttgcc tacggcgaac agcagtgcga aaactcgaac tgggtccgacc 480
ctccgcttgt tgcgatcgct taatggcaca aagtcgaatg ttttgccgcc tgtaaatgct 540
tctgacctct acgatgaaag ccaatcattg gctttgccta agacaccgat acagcgcccta 600
cacgaaccgg gacctttgga gacaacattg attaccaacg aagacactcc tgatcctttt 660
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gatcttggtg atacatatga cacccttgac aaggctgggt atcgatccaa ccctctgcaa 1560
gctccctcga agcaccctt ctatgagagc cagtatgaag aggagcatac tgcagcccag 1620
aatggctggc ttccagtggg ccagatagtt ccatccgacg taaccatccc cgaagacgac 1680
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<210> 2

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 2

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  20          25          30
Ala Asn His Phe Lys Leu Lys Leu Arg Thr Asp Asp Pro Asn Ser Val
  35          40          45
Lys Leu Leu Glu Arg Tyr Asp Gln Trp Phe Asp Asn Asn Gly Phe Ala
  50          55          60
Lys Leu Leu Ser Ala Arg Met Ala Ser Lys Glu Ser Arg Lys Lys Arg
  65          70          75          80
Lys Asp Glu Ala Ser Thr Ser Asn Thr Thr Lys Arg Thr Arg Ser Gln
  85          90          95
Ala Ser Ile Val Glu Thr Glu Gly Ser Ser Thr Pro Ala Met Pro Ala
  100         105         110
Thr Pro Asn Pro Asp Tyr Leu Asp Pro Arg Leu Ala Asp Ser His Asn
  115         120         125
Asp Asn Gln Gln His Ala Gly Thr Thr Leu Ala Ala Ser Ile Pro Asn
  130         135         140
Gln Leu Pro Thr Ala Asn Ser Ser Ala Lys Thr Arg Thr Gly Pro Thr
  145         150         155         160
Leu Arg Leu Leu Arg Ser Ser Asn Gly Thr Lys Ser Asn Val Leu Pro
  165         170         175
Pro Val Asn Ala Ser Asp Leu Tyr Asp Glu Ser Gln Ser Leu Ala Leu
  180         185         190
Pro Lys Thr Pro Ile Gln Arg Leu His Glu Pro Gly Pro Leu Glu Thr
  195         200         205
Thr Leu Ile Thr Asn Glu Asp Thr Pro Asp Pro Phe Val Asp Ser Gly
  210         215         220
Asp Gln Thr Gln Ala Ser Ala Glu Ala Glu Met Asp Lys Thr Arg Ala
  225         230         235         240
Glu Glu Ile Ser Arg Leu Lys Gly Val Leu Tyr Pro Gly Met Asp Ile
  245         250         255
Phe Asp Ser Ala Thr Val Gln Met Arg Arg Arg Arg Asn Gln Lys Lys
  260         265         270
Asp Ser Gly Val Leu Lys Thr Met Glu Glu Thr Ser Leu Leu Val Glu
  275         280         285
Pro Ser Glu Gln Val Tyr Ser Pro Gly Gly Thr Leu Leu Thr Glu Arg
  290         295         300
Met Ile Thr Gly Asn Val Glu Asp Tyr Ser Pro Leu Lys Gly Glu Thr
  305         310         315         320
Pro Ile Pro Lys Gly Gly Leu Thr Arg Thr Arg Ser Thr Arg Leu Thr

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				325					330					335			
Lys	Ala	Asp	Pro	Asn	Val	Ser	Arg	Ala	Ala	Asp	Arg	Lys	Arg	Gln	Lys		
			340					345					350				
Thr	Asp	Lys	Asp	Arg	Lys	Asn	Met	Ala	Asp	Glu	Gly	Ala	Asn	Glu	Glu		
		355				360						365					
His	Thr	Ser	Ser	Arg	Arg	Ser	Arg	Arg	Ala	Ala	Ala	His	Ser	Tyr	Val		
	370					375					380						
Gly	Asp	Asp	Glu	Glu	Ile	Gly	Leu	Thr	Val	Asn	Thr	Phe	Gly	Lys	Arg		
385					390					395					400		
Pro	Arg	Gly	Gly	Phe	Asp	Val	Phe	Val	Asp	Glu	Arg	Lys	Glu	Glu	Glu		
				405					410					415			
Asp	Ser	Lys	Thr	Thr	Tyr	Gln	Gln	Pro	Gly	Phe	Arg	Ala	Gln	Phe	Asp		
			420					425					430				
Thr	Leu	Thr	Pro	Thr	Arg	Leu	Val	Leu	Asn	Gly	Lys	Thr	Asn	Ala	Gly		
		435				440						445					
Ile	His	Ala	Pro	Arg	Ile	Gly	His	Ala	Ser	Leu	Ala	Lys	Glu	Asn	Ile		
	450					455					460						
Glu	Pro	Ile	Leu	Asn	Pro	Gln	Gly	Arg	Ile	Ala	Pro	His	Gly	Trp	Asn		
465				470						475					480		
Ser	Pro	Phe	Val	Lys	Tyr	Pro	Asp	Ser	Asp	Asp	Phe	Gly	Phe	Gly	Pro		
				485					490					495			
Ser	Tyr	Leu	Pro	Asp	Leu	Gly	Asp	Thr	Tyr	Asp	Thr	Leu	Asp	Lys	Ala		
			500					505					510				
Gly	Tyr	Arg	Ser	Asn	Pro	Leu	Gln	Ala	Pro	Ser	Lys	His	Pro	Phe	Tyr		
		515					520					525					
Glu	Ser	Gln	Tyr	Glu	Glu	Glu	His	Thr	Ala	Ala	Gln	Asn	Gly	Trp	Leu		
	530					535					540						
Pro	Val	Asp	Gln	Ile	Val	Pro	Ser	Asp	Val	Thr	Ile	Pro	Glu	Asp	Asp		
545					550					555					560		
Gln	Ile	Phe	Pro	Thr	Tyr	Tyr	Phe	Ser	Thr	Asp	Val	Asn					
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<210> 3
<211> 939
<212> DNA
<213> Artificial Sequence
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<220>  
<223> fungal gene

<400> 3						
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gcggagttcg	ccgtcgtcgc	caatctgcac	caccagcacg	tcgtctcgac	cttgcgaactc	240
ctccccatgc	gcggaggaaa	tctagccgct	tgcattggag	actgtgcggg	tggggatctt	300
cactccctga	tcacggtctg	tcctctgcac	agattaccct	cggaagaggc	agactgtctt	360
ttcaagcagc	ttcttctgtg	catctcctac	cttcacaaat	caggcatcgc	ccaccgcgac	420
ctgaagccgg	agaacctcct	cctgacacac	agggcttgcc	tcaagatctc	agactttgcg	480
aatgccgagc	gcgtccggtt	cgatggtgat	gattctcagc	atgccaatga	cctggccgaa	540
actgaacgcc	gcagcttaga	accgacaccg	tatcttgccc	cggagcgata	ccttgacgag	600
ggcgacaggt	acatgtccag	atccgacccc	agagccctcg	atatctgggc	cgcggtctgt	660
atatacgtcg	ctatgaggac	aggaaggaa	ctgtggaaag	cggcaacgga	gaaggacgag	720
ggcttcaggc	cagatgtcga	agagcgtaa	gccgagaaga	cgaatactgt	tatccaggat	780
tcgtgccatt	acgtgggcgc	caaaagtata	tacgcatagt	taagcactga	tcctgggaag	840
cgactctatc	cgactgaagt	tctttcctca	gagtggcttc	agaacattga	ctgctgtatc	900

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<210> 4

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 4

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Met Ala Leu Ile Thr Arg Lys Tyr Gly Glu Ile Arg Gln Ile Thr Gly
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Leu Ser Asp His Ala Val Ile Leu Gln Ser His Lys Val Gln Tyr Cys
 20           25           30
Pro Pro Leu Asp Arg Tyr Tyr Ala Ile Lys Val Phe Arg Arg Ser Pro
 35           40           45
Gly Gln Ser Thr Asp Glu Tyr Thr Lys Gln Val Asn Ala Glu Phe Ala
 50           55           60
Val Val Ala Asn Leu His His Gln His Val Val Ser Thr Phe Glu Leu
 65           70           75           80
Leu Pro Ile Gly Gly Gly Asn Leu Ala Ala Cys Met Glu Tyr Cys Ala
 85           90           95
Gly Gly Asp Leu His Ser Leu Ile Thr Ala Gly Pro Ser His Arg Leu
100           105           110
Pro Ser Glu Glu Ala Asp Cys Leu Phe Lys Gln Leu Leu Arg Gly Ile
115           120           125
Ser Tyr Leu His Lys Ser Gly Ile Ala His Arg Asp Leu Lys Pro Glu
130           135           140
Asn Leu Leu Leu Thr His Arg Ala Cys Leu Lys Ile Ser Asp Phe Ala
145           150           155           160
Asn Ala Glu Arg Val Arg Phe Asp Gly Asp Asp Ser Gln His Ala Asn
165           170           175
Asp Leu Ala Glu Thr Glu Arg Arg Ser Leu Glu Pro Thr Pro Tyr Leu
180           185           190
Ala Pro Glu Arg Tyr Leu Asp Glu Gly Asp Arg Tyr Met Ser Arg Ser
195           200           205
Asp Pro Arg Ala Leu Asp Ile Trp Ala Ala Ala Val Ile Tyr Val Ala
210           215           220
Met Arg Thr Gly Arg Asn Leu Trp Lys Ala Ala Thr Glu Lys Asp Glu
225           230           235           240
Gly Phe Arg Ala Tyr Val Glu Glu Arg Lys Ala Glu Lys Thr Asn Thr
245           250           255
Val Ile Gln Asp Ser Cys His Glu Arg Gly Arg Lys Val Ile Tyr Ala
260           265           270
Met Leu Ser Thr Asp Pro Gly Lys Arg Pro Ile Ala Thr Glu Ile Leu
275           280           285
Ser Ser Glu Trp Leu Gln Asn Ile Asp Cys Cys Ile Phe Asp His Ser
290           295           300
Gln Ala Glu Ser Asn Gly Phe Ser Ala
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<210> 5

<211> 1512

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 5

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tacttagcca tgcagttcga tcccagcaaa cccggtgctc gagaccctt tggccgaact 180
ggcggatacg gagcaaatgg tgcataccct aatgagccaa caccttcagg caaagttgtg 240
atccatcaact ttacctgtcg atccctgaca attggcagct ggaggcggat cggacaaaat 300
gccatggacc tggttgtttt ctactcccc gagaaaggcg gcatgacct ctatatcaac 360
aacgacgcag ccgatacaa aatcgaatat ccttctcct acatcaagaa cattacactt 420
gagtcgggcg atcaaggacc gcagcccaac ggtgcgcctc cacggcctac tggctctgtc 480
gttgaattga accgaccgcc cctcttttac atggattcct ccaactcggg tggtttctac 540
cagtgcggcg actttacgga agaccaacaa gctagctcgg taatgattca tcgccttggc 600
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aaccgtctcg cgtatggcaa ctcccggca aacaactcta tgtcgccgcc tttcattcaa 720
cgccagctt cgcagccaaa tcaattcgcc cctgctttta tgagtatgta tgcggagaat 780
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gtgggcctcg aaggcaatgc atttgacttg ccgatgcact ccattgtctg gcattgttcg 1440
cccgcgctcc aggtgacta tcaaggaata gcaactggaa atgtcgatcc gaatgtttt 1500
actccggct ct 1512

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&lt;210&gt; 6

&lt;211&gt; 504

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 6

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Met Thr Glu Arg Ser Val Gln Ile Trp Phe Gln Asn Arg Arg Ala Lys
 1           5           10           15
Ile Lys Met Leu Ala Lys Lys Ser Ile Glu Thr Gly Glu Gly Cys Asp
      20           25           30
Ser Ile Pro Glu Ser Met Arg Gln Tyr Leu Ala Met Gln Phe Asp Pro
      35           40           45
Ser Lys Pro Gly Ala Arg Asp Pro Phe Gly Arg Thr Gly Gly Tyr Gly
      50           55           60
Ala Asn Gly Ala Tyr Pro Asn Glu Pro Thr Pro Ser Gly Lys Val Val
      65           70           75           80
Ile His His Phe Thr Cys Arg Ser Leu Thr Ile Gly Ser Trp Arg Arg
      85           90           95
Ile Gly Gln Asn Ala Met Asp Leu Val Val Phe Tyr Ser Pro Glu Lys
      100          105          110
Ala Cys Met Thr Tyr Tyr Ile Asn Asn Asp Ala Ala Gly Tyr Lys Ile
      115          120          125

```

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Glu Tyr Pro Phe Ser Tyr Ile Lys Asn Ile Thr Leu Glu Ser Gly Asp
 130          135          140
Gln Gly Pro Gln Pro Asn Gly Ala Pro Pro Arg Pro Thr Gly Leu Val
145          150          155          160
Val Glu Leu Asn Arg Pro Pro Leu Phe Tyr Met Asp Ser Ser Asn Ser
          165          170          175
Gly Gly Phe Tyr Gln Cys Gly Asp Phe Thr Glu Asp Gln Gln Ala Ser
          180          185          190
Ser Val Met Ile His Arg Leu Gly Gly His Pro Lys Val Leu Ser Val
          195          200          205
Gln Leu Ala Lys Leu Val Ser Leu Glu Ser Phe Gln Asn Arg Leu Ala
          210          215          220
Tyr Gly Asn Phe Pro Ala Asn Asn Ser Met Ser Pro Pro Phe Ile Gln
225          230          235          240
Arg Pro Ala Ser Gln Pro Asn Gln Phe Ala Pro Ala Phe Met Ser Met
          245          250          255
Tyr Ala Glu Asn Pro Ala Val Met Asn Leu Gln Ala Ala Arg Gly His
          260          265          270
Lys Arg Gln Arg Ser Arg Ser Val Pro Val Ala Ile Asp Phe Ser Ala
          275          280          285
Leu Gly Ala Pro Met Thr Gln Phe Ser Met Pro Gln Ala Gln Gln Phe
          290          295          300
Ser Gln Ala Asp Ser Gly Ile Tyr Ala Pro Ile Pro Gln Ser Thr His
305          310          315          320
Ser Leu Ala Ala Asn Leu Arg Ile Asp Thr Ser Ser Gly Tyr Ala Phe
          325          330          335
Asp Pro Arg Ala His Pro Met Ser Ala Thr Thr Thr Ala Ser Pro Ser
          340          345          350
Asp Phe Ala Ser Pro Ala Leu Phe Ser Ala Gly Pro Gln Gly Asp Ser
          355          360          365
Thr Pro Val Gly Ser Val Gly Ala Gln Phe Thr Leu Pro Tyr Val Ser
          370          375          380
Pro Ala Val Asp Ser Gly Val Ser Thr Gln Ala Ala Ser Pro Tyr Ser
385          390          395          400
Asn Val Ser His Val Asp Pro Met Ile Ala Asn His Ser Pro Pro Leu
          405          410          415
Thr Asn Met Ser His Thr Pro His Asp Val Tyr Gly Met Gly Ser Glu
          420          425          430
His Gln Pro Ser Tyr Thr Glu Glu Gly Met Pro Met Gly Gly Gly Met
          435          440          445
Tyr Lys His Ile Asn Phe Ser Ser Val Pro Thr Thr Val Gly Leu Glu
          450          455          460
Gly Asn Ala Phe Asp Leu Pro Met His Ser Met Ser Gly His Ala Ser
465          470          475          480
Pro Gly Val Gln Gly Asp Tyr Gln Gly Ile Ala Leu Glu Asn Val Asp
          485          490          495
Pro Asn Val Leu Thr Pro Gly Ser
          500

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&lt;210&gt; 7

&lt;211&gt; 1557

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 7

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cctcttctct ctgtctcccat ctcgagcatg ccaatgcctc agtacacgat gcagcctcag 120
taccaggtct ctgagccgca caccctgcct cctctgcaac cccatcatag ccagtcgccc 180
gctctcact cgtacatggg gcagccgccc taccggcctg atctgaacag gtaccccgca 240
tcaagtcacg atgtttacgc gtcttctgct gcgcccataa tgccccacac taccgtgggc 300
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caggggagc gcggtatct tccgagtgt ccgggacgc caactccgt cacaatggt 660
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tgcccgaact gtaacaagac ttatcttcat gccaaagcat tcaagcgcca tctgctacgc 780
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cacttgctgc accccaatgc gcatgtgaag aggtcccaac agcaggctg gccgaatcct 960
gtaaaacctg tccaggatga agtcagtagt accgtccgc ctcccaatgg catcccgggc 1020
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cctgaagacg cgtttcccgc cgccggccg catcaaggag ccccttgcc acaagctccc 1200
aagcagagcc cgtatctcgt gcagccgggt gctgaccct ctggccacca gttgaatatt 1260
gaccgaaaca tcgagcaggt aaaacaaccg gttgttcaag accccaagcg cctgtgatg 1320
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&lt;210&gt; 8

&lt;211&gt; 519

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 8

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Met Asp Pro Arg Asn His Pro Ser Arg Pro Pro Ser Thr Ser Leu Pro
 1           5           10           15
Gln Gly Ser Ala Pro Leu Pro Ser Ala Pro Ile Ser Ser Met Pro Met
          20           25           30
Pro Gln Tyr Thr Met Gln Pro Gln Tyr Pro Val Ser Gln Pro His Thr
          35           40           45
Leu Pro Pro Leu Gln Pro His His Ser Gln Ser Pro Ala Pro His Ser
          50           55           60
Tyr Met Gly Gln Pro Pro Tyr Arg Pro Asp Leu Asn Arg Tyr Pro Ala
65           70           75           80
Ser Ser His Asp Val Tyr Ala Ser Ser Ala Ala Pro Ile Met Pro His
          85           90           95
Thr Thr Val Gly Ser Leu Pro Pro Thr Ser Phe Leu Ser His Pro Asn
          100          105          110
Pro Gln Ala Gln Ala Gln Ala Gln Ser Pro His Tyr Pro Pro Pro
          115          120          125
His Ser Val Leu Pro Pro Ala Ser Ser Ala Gln Ser Tyr Pro Gln Pro
          130          135          140
Ile Ala Pro Ala Pro Pro Arg Asp Arg Arg Ala Asp Phe Asn Asn Gly

```

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145          150          155          160
Leu Pro Ser Gly Ala Phe Ser Tyr Ser Asp Gly Lys Pro Gln Gly Trp
165          170          175
Asp Pro Val Ala Ala Asn Gly Ala Ala Pro Tyr Pro Gly Lys Asp Ser
180          185          190
Pro Arg Thr Gln Val Val Gly Ser Gln Gly Arg Arg Gly Ile Leu Pro
195          200          205
Ser Val Pro Gly Arg Ala Thr Pro Val Thr Asn Gly Val Asn Gly Thr
210          215          220
Gly Lys Asn Thr Thr Ile Pro Ala Lys Asp Ala Asp Gly Lys Phe Pro
225          230          235
Cys Pro Asn Cys Asn Lys Thr Tyr Leu His Ala Lys His Leu Lys Arg
245          250          255
His Leu Leu Arg His Thr Gly Asp Arg Pro Tyr Met Cys Val Leu Cys
260          265          270
Lys Asp Thr Phe Ser Arg Ser Asp Ile Leu Lys Arg His Phe Gln Lys
275          280          285
Cys Ser Ile Arg Arg Gly Asn Pro Thr Gly Ala Thr His Leu Ser His
290          295          300
Pro Asn Ala His Val Lys Arg Ser Gln Gln Gln Ala Ala Ala Asn Pro
305          310          315
Val Lys Pro Val Gln Asp Glu Val Ser Ser Thr Val Pro Pro Pro Asn
325          330          335
Gly Ile Pro Gly Thr Thr Tyr Gly Glu Gly Ala Val Asn Gly Asn Gly
340          345          350
Leu Ala Pro Ala Arg Pro Gly Tyr Ala Asp His Gln Thr Met Gly Phe
355          360          365
Pro Met Ser Ser Val Asn Gly Met Gly Arg Gly Gln Pro Glu Asp Ala
370          375          380
Phe Pro Gly Gly Arg Pro His Gln Gly Ala Pro Trp Pro Gln Ala Pro
385          390          395
Lys Gln Ser Pro Tyr Leu Val Gln Pro Gly Ala Asp Pro Ser Gly His
405          410          415
Gln Leu Asn Ile Asp Arg Asn Ile Glu Gln Val Lys Gln Pro Val Val
420          425          430
Gln Asp Pro Lys Arg Pro Val Met Pro Gly His Pro Gly His Pro Gly
435          440          445
Glu Leu Asp Trp Thr Ser Met Phe Gln Pro Gln Ala Pro Glu Gly Tyr
450          455          460
Met Phe Ser Gln Ser Met Pro Gly Gly Gln Glu Pro Ile His Ala His
465          470          475
Val Glu Thr Glu Arg Lys Tyr Tyr Pro Thr Thr Thr Ala Gly Gln Glu
485          490          495
Ser Gly Met Asn Gly Leu Tyr Leu Ala Ser Thr Met Ser Gly Asp Gly
500          505          510
Thr Val Gln Pro Ala Arg Gln
515

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&lt;210&gt; 9

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene



&lt;400&gt; 9

```

atgattaatg agacgcagga gattcactcc gagaacgaca tcgacagagc gccgatgcga 60
tcgtcgattg agctgccttc tctccgtgat cacttcaaac gggactcgtt gcctccattt 120
tcgtcccttc aacctagatc gtccttacct tcgattctca accactctcc tcccggtcgc 180
tcttcgaccc ttccgccgat ccagcggacg aacaagcttc cccgacctcg caaaggatcg 240
ataaccgggg cgcgaaaagc caagcatgaa cggtcgaggt cgaaagagtt tggtaggcgc 300
ccgagcatag gcgataggaa ggctctatca gcagaaccgc aaaccgctgc ctggg'gcgag 360
ggcaagcgtt gggaggatct cattgaggcg gccacatcag caaccgaggt tgatgacgac 420
agacagtcag agttggggcg ttcaccaacc attccaccaa ccattccgaa tatcgcttcg 480
atcacatcgg caccatcaat caaaagccga tcatccatgc cgctgcctt ccaatcccct 540
ggggtacccc cacctgcata gcatcgcccg ttccccacca catcatatgc agcgtcgccc 600
ttgcacaaat ctttgacccc gccgccttat gaattctccc gcaaccgtga cgccgaccta 660
gaaccttttc cctccattga atcgtctttg gactcagcat cgacaacatc tggaaaagcac 720
ttttactcca accacttgaa ccccgccaga aatccagatt cgagtccagt gttaaactta 780
tttccatctt ccgcagccca gcgacaacac caccgcttct ctaatcccac cccggcgtct 840
ttccgtagca gggagataca gatcttctgc gccagctgca agcaggcatg gcctctcaat 900
gaatgctatg cctgtactga atgtatctgc ggggtatgcc gcgattgcgt cggaagtgtc 960
atgagcagtc cgcctgcgac gttcaagaac gtgacatcca gccctgggag cgcaatgtca 1020
cacggcccga caagctatcc gagtccgaac ccacgtgggt gccacgctg ccacaccgtg 1080
ggagggaagt ggaaagcatt ccaactggac atcaaa 1116

```

&lt;210&gt; 10

&lt;211&gt; 372

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 10

```

Met Ile Asn Glu Thr Gln Glu Ile His Ser Glu Asn Asp Ile Asp Arg
 1             5             10             15
Ala Pro Met Arg Ser Ser Ile Glu Leu Pro Ser Leu Arg Asp His Phe
      20             25             30
Lys Arg Asp Ser Leu Pro Pro Phe Ser Ser Pro Gln Pro Arg Ser Leu
      35             40             45
Leu Pro Ser Ile Leu Asn His Ser Pro Pro Gly Arg Ser Ser Thr Leu
      50             55             60
Pro Pro Ile Gln Arg Thr Asn Lys Leu Pro Arg Pro Arg Lys Gly Ser
      65             70             75             80
Ile Thr Gly Ala Arg Lys Ala Lys His Glu Arg Ser Arg Ser Lys Glu
      85             90             95
Phe Gly Arg Arg Pro Ser Ile Gly Asp Arg Lys Ala Leu Ser Ala Glu
      100            105            110
Pro Gln Thr Ala Ala Trp Ala Gln Gly Lys Arg Trp Glu Asp Leu Ile
      115            120            125
Glu Ala Ala Thr Ser Ala Thr Glu Val Asp Asp Asp Arg Gln Ser Glu
      130            135            140
Leu Gly Arg Ser Pro Thr Ile Pro Pro Thr Ile Pro Asn Ile Ala Ser
      145            150            155            160
Ile Thr Ser Ala Pro Ser Ile Lys Ser Arg Ser Ser Met Pro Pro Ala
      165            170            175
Phe Gln Ser Pro Gly Leu Pro Pro Pro Ala Ser His Arg Pro Phe Pro
      180            185            190
Pro Thr Ser Tyr Ala Ala Ser Pro Leu His Lys Ser Leu Thr Pro Pro
      195            200            205
Pro Tyr Glu Phe Ser Arg Asn Arg Asp Ala Asp Leu Glu Pro Phe Pro

```

210	215	220
Ser Ile Glu Ser Ser	Leu Asp Ser Ala Ser Thr	Thr Ser Gly Lys His
225	230	235
Phe Tyr Ser Asn His	Leu Asn Pro Ala Arg Asn	Pro Asp Ser Ser Pro
245	250	255
Val Leu Asn Leu Phe	Pro Ser Ser Ala Ala Gln Arg	Gln His His Arg
260	265	270
Phe Ser Asn Pro Thr	Pro Ala Ser Phe Arg Ser Arg	Glu Ile Gln Ile
275	280	285
Phe Cys Ala Ser Cys	Lys Gln Ala Trp Pro Leu Asn	Glu Cys Tyr Ala
290	295	300
Cys Thr Glu Cys Ile	Cys Gly Val Cys Arg Asp	Cys Val Gly Ser Phe
305	310	315
Met Ser Ser Pro Pro	Ala Thr Phe Lys Asn Val Thr	Ser Ser Pro Gly
325	330	335
Ser Ala Met Ser His	Gly Pro Thr Ser Tyr Pro Ser	Pro Asn Pro Arg
340	345	350
Gly Cys Pro Arg Cys	His Thr Val Gly Gly Lys Trp	Lys Ala Phe Gln
355	360	365
Leu Asp Ile Lys		
370		

<210> 11  
 <211> 933  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 11  
 atgacggcgc gccaatcaac accgtcctcc gacaactcgc actcagacag cggcgtccgc 60  
 aagcgagtat gcaaggcttg cgatcggttg cgactgaaaa agtccaagtg tgacggagcc 120  
 aaaccatgcg gtgcgtgtcg agcagacaac acgctctgtg ttttcggcga gaggaagaaa 180  
 gctcatgaca aagtgtaccc taagggggtat gttgagatgc tggacaaca acaaacttgg 240  
 ctagtcaatg gcttgcaaga actgtatcgc cgccttcttg agggatgatg atggccgggc 300  
 gagccgctga aatgcgaagc gaacgggcag cccttgacac acgatctctt gacgcagctc 360  
 ggcgctctcg acacaagcaa gcacgagcgg ttcgaagaac acgccgaggt catgcagcag 420  
 gaattatgga agcgaaatgc cggacacatg cagcgccagg actcatcaga taccagctcc 480  
 gagagcccac agtcgcccgt catgcgctct caattctcag atcccttttc tgtgocgaca 540  
 gtaccacaaa ctccgacaac gatcagcccg aacacgacgc tgcgaataga cgtcccgcga 600  
 tcagcgacga agagtgaacc gcagatgaca tcgccaaact ccatatacac cacagccgtg 660  
 tccatgcccg gagtggtcga cccgtctgag ctgcagagcg cccaaatagc aaaccgcgag 720  
 tggcccagcc ctggcttttg aggctacgac gaaatggacc tgatgtcttg gcaatacaat 780  
 ggtctgccat acgaagatgc gatctcctcg ccaatgttca atcgccaat gccaatgggg 840  
 tgcctgatac cagggtcata cggaacttg gataacaaga acgactttga ggatatcaac 900  
 caatttctga acacacagtt ggagattacg tcg 933

<210> 12  
 <211> 311  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

&lt;400&gt; 12

```

Met Thr Ala Arg Gln Ser Thr Pro Ser Ser Asp Asn Ser His Ser Asp
 1          5          10          15
Ser Gly Val Arg Lys Arg Val Cys Lys Ala Cys Asp Arg Cys Arg Leu
          20          25          30
Lys Lys Ser Lys Cys Asp Gly Ala Lys Pro Cys Gly Arg Cys Arg Ala
          35          40          45
Asp Asn Thr Leu Cys Val Phe Gly Glu Arg Lys Lys Ala His Asp Lys
          50          55          60
Val Tyr Pro Lys Gly Tyr Val Glu Met Leu Glu Gln Gln Gln Thr Trp
65          70          75          80
Leu Val Asn Gly Leu Gln Glu Leu Tyr Arg Arg Leu Leu Glu Gly Asp
          85          90          95
Gly Trp Pro Gly Glu Pro Leu Lys Cys Glu Ala Asn Gly Gln Pro Leu
          100          105          110
Thr His Asp Leu Leu Thr Gln Leu Gly Ala Leu Asp Thr Ser Lys His
          115          120          125
Glu Arg Phe Glu Glu His Ala Glu Val Met Gln Gln Glu Leu Trp Lys
          130          135          140
Arg Asn Ala Gly His Met Gln Arg Gln Asp Ser Ser Asp Thr Ser Ser
145          150          155          160
Glu Ser Pro Gln Ser Pro Val Met Pro Ser Gln Phe Ser Asp Pro Phe
          165          170          175
Ser Val Arg Thr Val Pro Gln Thr Pro Thr Thr Ile Ser Pro Asn Thr
          180          185          190
Thr Leu Arg Ile Asp Val Pro Gln Ser Ala Thr Lys Ser Glu Pro Gln
          195          200          205
Met Thr Ser Pro Asn Ser Ile Tyr Thr Thr Ala Val Ser Met Pro Arg
          210          215          220
Val Val Asp Pro Ser Glu Leu Gln Ser Ala Gln Ile Ala Asn Pro Gln
225          230          235          240
Trp Pro Ser Pro Gly Phe Gly Gly Tyr Asp Glu Met Asp Leu Met Ser
          245          250          255
Gly Gln Tyr Asn Gly Leu Pro Tyr Glu Asp Ala Ile Ser Ser Pro Met
          260          265          270
Phe Asn Arg Pro Met Pro Met Gly Cys Leu Ile Pro Gly Ser Tyr Gly
          275          280          285
Asn Leu Asp Asn Lys Asn Asp Phe Glu Asp Ile Asn Gln Phe Leu Asn
          290          295          300
Thr Gln Leu Glu Ile Thr Ser
305          310

```

&lt;210&gt; 13

&lt;211&gt; 660

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 13

```

atgtcgcagc ccatacgcctg ccctccaatg gagcactcgc cctcctcctt gtcctcctac 60
tcctcttact cccccagttc gtcctactcc gccgtgagcg acgactcggg catgagcatg 120
ttggacatgt acttccctgca cggtggccgt ggacacggcg ccagcccccgg cacaagcacg 180
gggtcccgga gcgtcgtcga tttcccgttc agccagcaat cgttcgattt cgagccttcg 240
tcgctggaca gcaatggccc ctacttcgag ttcaaccgga ctttcgtata cacacccgag 300

```

```

gcgtttcccg tcatggacgc cccgacctcc taccggcgga gctcgaaccc ggccctggctcg 360
ccaacctcca tgcttgctga gcagtcgata tttcctctcg acgggcttag ccaagaacca 420
gtcaagccag ccaaacccta cagctgcgaa gattgcggca aggccttcac ccgcccagcg 480
gacctaaagc gccaccatag cactgtacac taccgggttt tccagaactg ccctgtaccg 540
gactgctcgc gcaaggacaa ccatggcttt ccgcggcgcg accacctcgt cgagcacctg 600
cgctcgtacc accacatgga tgtgccgaag cggcgcgcag caaagcgatt gagaactgtt 660

```

<210> 14  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 14
Met Ser Gln Pro Ile Ala Cys Pro Pro Met Glu His Ser Pro Ser Ser
 1           5           10           15
Leu Ser Ser Tyr Ser Ser Tyr Ser Pro Ser Ser Ser Tyr Ser Ala Val
      20           25           30
Ser Asp Asp Ser Gly Met Ser Met Leu Asp Met Tyr Phe Leu His Gly
      35           40           45
Gly Arg Gly His Gly Ala Ser Pro Gly Thr Ser Thr Gly Pro Gly Ser
      50           55           60
Val Val Asp Phe Pro Phe Ser Gln Gln Ser Phe Asp Phe Glu Pro Ser
      65           70           75           80
Ser Leu Asp Ser Asn Gly Pro Tyr Phe Glu Phe Asn Pro Thr Phe Val
      85           90           95
Tyr Thr Pro Glu Ala Phe Pro Val Met Asp Ala Pro Thr Ser Tyr Pro
      100          105          110
Ala Ser Ser Asn Pro Ala Trp Ser Pro Thr Ser Met Leu Val Glu Gln
      115          120          125
Ser Ile Phe Pro Leu Asp Gly Leu Ser Gln Glu Pro Val Lys Pro Ala
      130          135          140
Lys Pro Tyr Ser Cys Glu Asp Cys Gly Lys Ala Phe Thr Arg Pro Ala
      145          150          155          160
Asp Leu Lys Arg His His Ser Thr Val His Tyr Pro Val Phe Gln Asn
      165          170          175
Cys Pro Val Pro Asp Cys Ser Arg Lys Asp Asn His Gly Phe Pro Arg
      180          185          190
Arg Asp His Leu Val Glu His Leu Arg Ser Tyr His His Met Asp Val
      195          200          205
Pro Lys Arg Arg Ala Ala Lys Arg Leu Arg Thr Val
      210          215          220

```

<210> 15  
 <211> 684  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 15
atgcttgccg agaataacat ccagaaccag cagcagcagc agatgatgca gcagcagcag 60

```

```

cagcaacaac aacaacaaca acaacaacaa aatcaccaga atcaacaaca gaagtttgcc 120
aatccccagg cataccaggc tcagatgatg cgcgcgcaac tcatgcagat gcagctcgcc 180
caacagcagc agcaacaaag gcaacagcaa tcacaacagc agcaacaagc gcagccgcaa 240
ggccagcaac agccacagca tcaacaagga caaatgcttc aaaacagccc tcagctcaac 300
gcccagcaac agcagatggt gatggcagcg gcacaagcta acggcggcca actcccgcaa 360
aacatgcagg gcatgggtat gcagccgcga atgagtactc cagcgcggta caaccagctc 420
tatcagcagc ggcttttgag actacggcaa gacatggcta cgcgtctgat gccacagtac 480
ggaccaccca cgcaatatcc gccacagggt gcgcaggagt acagtgttgg ccttgaaaac 540
gctgctaagg gcttcgtgca agacctcatt cgcaggagc gtgtcgagtt tgctgctgct 600
caacagcgac aagcccaggc tgctgcccac gccaggcag tgcagcaaca gcagcacaac 660
atgatgcaga atggaatggg caag                                     684

```

<210> 16  
 <211> 228  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 16

Met	Leu	Ala	Gln	Asn	Asn	Ile	Gln	Asn	Gln	Gln	Gln	Gln	Gln	Met	Met
1				5					10					15	
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Asn	His
			20					25					30		
Gln	Asn	Gln	Gln	Gln	Lys	Phe	Ala	Asn	Pro	Gln	Ala	Tyr	Gln	Ala	Gln
		35					40					45			
Met	Met	Arg	Ala	Gln	Leu	Met	Gln	Met	Gln	Leu	Ala	Gln	Gln	Gln	Gln
	50					55					60				
Gln	Gln	Arg	Gln	Gln	Gln	Ser	Gln	Gln	Gln	Gln	Ala	Gln	Pro	Gln	
65					70				75					80	
Gly	Gln	Gln	Gln	Pro	Gln	His	Gln	Gln	Gly	Gln	Met	Leu	Gln	Asn	Ser
				85					90					95	
Pro	Gln	Leu	Asn	Ala	Gln	Gln	Gln	Gln	Met	Leu	Met	Ala	Ala	Ala	Gln
			100					105					110		
Ala	Asn	Gly	Gly	Gln	Leu	Pro	Gln	Asn	Met	Gln	Gly	Met	Gly	Met	Gln
		115					120					125			
Pro	Arg	Met	Ser	Thr	Pro	Ala	Arg	Tyr	Asn	Gln	Leu	Tyr	Gln	Gln	Arg
	130					135					140				
Leu	Leu	Arg	Leu	Arg	Gln	Asp	Met	Ala	Thr	Arg	Leu	Met	Pro	Gln	Tyr
145					150				155					160	
Gly	Pro	Pro	Thr	Gln	Tyr	Pro	Pro	Gln	Val	Ala	Gln	Glu	Tyr	Ser	Val
			165					170						175	
Gly	Leu	Glu	Asn	Ala	Ala	Lys	Gly	Phe	Val	Gln	Asp	Leu	Ile	Arg	Arg
		180					185						190		
Glu	Arg	Val	Glu	Phe	Ala	Ala	Ala	Gln	Gln	Arg	Gln	Ala	Gln	Ala	Ala
		195					200					205			
Ala	His	Ala	Gln	Ala	Val	Gln	Gln	Gln	Gln	His	Asn	Met	Met	Gln	Asn
	210					215					220				
Gly	Met	Gly	Lys												
225															

<210> 17  
 <211> 906  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 17

```

atgaacaacg acttcatgca aaacaacatt cgcagcgccc aggatgtgga acagattatt 60
tccaacatcc gattctccgg catgacgcct ctaggttccg ctctgagatc caaggtactt 120
gatcccatga tagtgggtcc agccagagca ggcgcctgc aaaagccggt tctcgtcatc 180
actatcaccg atggtcagcc cgctggagaa cctctggact ccgtcgctca ggggaattcgc 240
tacgctgttg atgaggtttc gagatcccca tttggacgtg gtgcggttgc cttccagttc 300
tcgcaagtcg gaaacgacac caaggctcgg gacttcctcg gcagtctcga caacgaccct 360
agcattggtg gcctgatcga ctgcacctcc aactttgaag tagaacagga tgagatgtcc 420
cgtgctaacc cacctgtgca tctgactcgt gagctgtggt gcgcgaaact catgctcggc 480
tctatcgatt cctcgtacga taccaaggac gagaggggta gtggcccatc tgggtctcct 540
cctgggcctc ctctggcca gtacggcggc tatggtcagt caggaccggg atacggctca 600
tccgcaccat acaatcccg ccagcaacag ccgtacagcc ctgcttacc cccgcacagc 660
caagcgctg gaggtatgc acagccacct cccaaggcc agtacggcg ctatagccaa 720
ccgggcccg gatatggctc acccgcgctc tacagctccg gacaacaaca ggggtatggc 780
tctgctcctt acccaccgag cagccaagcg tctgggagct atggccagca acaatatgga 840
caacggcccg gatctcagcc tggttatccc ggtcaacagc ctccgtacgg acagcagccg 900
aggtat

```

&lt;210&gt; 18

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 18

```

Met Asn Asn Asp Phe Met Gln Asn Asn Ile Arg Ser Ala Gln Asp Val
1      5      10      15
Glu Gln Ile Ile Ser Asn Ile Arg Phe Ser Gly Met Thr Pro Leu Gly
20      25      30
Ser Ala Leu Arg Ser Lys Val Leu Asp Pro Met Ile Val Gly Pro Ala
35      40      45
Arg Ala Gly Arg Leu Gln Lys Pro Val Leu Val Ile Thr Ile Thr Asp
50      55      60
Gly Gln Pro Ala Gly Glu Pro Leu Asp Ser Val Ala Gln Gly Ile Arg
65      70      75      80
Tyr Ala Val Asp Glu Val Ser Arg Ser Pro Phe Gly Arg Gly Ala Val
85      90      95
Ala Phe Gln Phe Ser Gln Val Gly Asn Asp Thr Lys Ala Arg Asp Phe
100     105     110
Leu Gly Ser Leu Asp Asn Asp Pro Ser Ile Gly Gly Leu Ile Asp Cys
115     120     125
Thr Ser Asn Phe Glu Val Glu Gln Asp Glu Met Ser Arg Ala Asn Pro
130     135     140
Pro Val His Leu Thr Arg Glu Leu Trp Cys Ala Lys Leu Met Leu Gly
145     150     155     160
Ser Ile Asp Ser Ser Tyr Asp Thr Lys Asp Glu Arg Gly Ser Gly Pro
165     170     175
Ser Gly Ala Pro Pro Gly Pro Pro Pro Gly Gln Tyr Gly Gly Tyr Gly
180     185     190
Gln Ser Gly Pro Gly Tyr Gly Ser Ser Ala Pro Tyr Asn Pro Gly Gln
195     200     205

```

```

Gln Gln Pro Tyr Ser Pro Ala Tyr Pro Pro His Ser Gln Ala Pro Gly
 210          215          220
Gly Tyr Ala Gln Pro Pro Gln Gly Gln Tyr Gly Gly Tyr Ser Gln
225          230          235          240
Pro Gly Pro Gly Tyr Gly Ser Pro Ala Pro Tyr Ser Ser Gly Gln Gln
          245          250          255
Gln Gly Tyr Gly Ser Ala Pro Tyr Pro Pro Ser Ser Gln Ala Ser Gly
          260          265          270
Ser Tyr Gly Gln Gln Gln Tyr Gly Gln Arg Pro Gly Ser Gln Pro Gly
          275          280          285
Tyr Pro Gly Gln Gln Pro Pro Tyr Gly Gln Gln Pro Arg Tyr
          290          295          300

```

<210> 19  
 <211> 810  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 19
atgactagcc gtcagaatga atacttcacg cccggagatg gtattagccg agaagtaatt 60
caggccgaca tctgccgtta ccttggaat gatgctttag taagacctgg aaaccacaat 120
ggtcgcgcgg gattcttcat tcgcgcttat cgaaacctca catcagaaat gattgctgat 180
ctcaaggcgg actccgcccg ctgggaagca gacgtcagaa gtcgtgctga ccaaggttat 240
ccccggggca gctacatcca ggactacagc tactctcaac ctagccgggc tacaccaacc 300
tactcaacct ctatgggaag ttccatgcac cctgaaatgt cccatggtca aggcccttct 360
cctcctacaa cctacgctgc tccgcgcgag cagtattctg agcagtatca ccaatctggc 420
taccagcaaa cttcaagtcc gtcatactca aatgctccgt catatccttc aaaccactcg 480
ggctttggat ctggtcagcc cccataccct caacatatcc cctacagtgc tccaacccag 540
cctcctgtga cttctgaggt ccacccttca tatacttaag ccagctctgg ctatggtttc 600
gagaatgggc gaaacaatgc ccctcggtac cctggtcctg gatatgatgc cgattctgat 660
tattctcctg ttactaccgg aatggcttat cctgctacca ctgccctga tccacggata 720
ggaatggagc ccagatacac accggagtcc acatatgacc gcagtaggcc gcagccagca 780
agagaaagag aggcctccccg ccgaacgcgg          810

```

<210> 20  
 <211> 270  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 20
Met Thr Ser Arg Gln Asn Glu Tyr Phe Ile Pro Gly Asp Gly Ile Ser
 1          5          10          15
Arg Glu Val Ile Gln Ala Asp Ile Cys Arg Tyr Leu Gly Asn Asp Ala
          20          25          30
Leu Val Arg Pro Gly Asn His Asn Gly Arg Ala Gly Phe Phe Ile Arg
          35          40          45
Ala Tyr Arg Asn Leu Thr Ser Glu Met Ile Ala Asp Leu Lys Ala Asp
          50          55          60
Ser Ala Arg Trp Glu Ala Asp Val Arg Ser Arg Ala Asp Gln Gly Tyr
65          70          75          80

```

Pro	Arg	Gly	Ser	Tyr	Ile	Gln	Asp	Tyr	Ser	Tyr	Ser	Gln	Pro	Ser	Arg
			85					90					95		
Ala	Thr	Pro	Thr	Tyr	Ser	Thr	Ser	Met	Gly	Ser	Ser	Met	His	Pro	Glu
			100					105					110		
Met	Ser	His	Gly	Gln	Gly	Pro	Ser	Pro	Pro	Thr	Thr	Tyr	Ala	Ala	Pro
		115					120					125			
Pro	Gln	Gln	Tyr	Ser	Glu	Gln	Tyr	His	Gln	Ser	Gly	Tyr	Pro	Ala	Thr
		130				135					140				
Ser	Ser	Pro	Ser	Tyr	Ser	Asn	Ala	Pro	Ser	Tyr	Pro	Ser	Asn	His	Ser
145				150					155					160	
Gly	Phe	Gly	Ser	Gly	Gln	Pro	Pro	Tyr	Pro	Gln	His	Ile	Pro	Tyr	Ser
			165					170						175	
Ala	Pro	Thr	Gln	Pro	Pro	Val	Thr	Ser	Glu	Val	His	Pro	Ser	Tyr	Thr
		180					185					190			
Tyr	Ala	Ser	Ser	Gly	Tyr	Gly	Phe	Glu	Asn	Gly	Arg	Asn	Asn	Ala	Pro
		195				200					205				
Arg	Tyr	Pro	Gly	Pro	Gly	Tyr	Asp	Ala	Asp	Ser	Asp	Tyr	Ser	Pro	Val
	210				215						220				
Thr	Thr	Gly	Met	Ala	Tyr	Pro	Ala	Thr	Thr	Ala	Pro	Asp	Pro	Arg	Ile
225					230					235				240	
Gly	Met	Glu	Pro	Arg	Tyr	Thr	Pro	Glu	Ser	Thr	Tyr	Asp	Arg	Ser	Arg
			245					250					255		
Pro	Gln	Pro	Ala	Arg	Glu	Arg	Glu	Ala	Pro	Arg	Arg	Thr	Arg		
		260					265					270			

&lt;210&gt; 21

&lt;211&gt; 2082

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 21

```

atgacacacc gagattccga cttccgtcat caactgggca agtttcgact cgataccctg 60
ccgtcgcccg ctgtcgctgc tgctgctgca ccccgcgtca tctcctccac ctccatcctc 120
tccagcccca acacgaccac caccaccacc accacaacaa cttcctcctc gggccccgtc 180
cgaagcaaaa gagtctccac cgctcgcat ttctgtcgca aacgcaagaa gaaatgtgac 240
tttcgttata ccaattgttc cgctgtacg cgcgccggcg tgcgatgtac cattccacca 300
cccggccctc aggtcgccag cgctccgtc cctcgatgc agctggaaac tctgcaaaat 360
cgcgctccgat ggctggaaga cgtggtgogc cggaagacgg gcatctctgt cgccgatcgg 420
cccacgggga cgccgctcga tggcgagggc gacccggact ggtggtacca ggtgccggcc 480
ttgatgatga cccgggacaa cctctcccgc acggcgccgg ggacgaccgc gggaggcgctc 540
acctccagcc cgtctacctc gtctccatcc gccgtgggac ccgaattgcc caatgtcggc 600
gaaactttcc ggcaccagct ggagcatcgt cgaccgtccg tggctcgtcc cgtcgctcgc 660
gccccgcgcg tgctcgact cgctcgctg gcggagggcg aacgcgtagc cgcacagtac 720
ttcgatagca tgggctatca atatcccttt ctccatcgcg gggatttctc cgcgcagttg 780
cgatcgcttt atacctccga cagcgctggt gcccgaggag tccactatac ctaccacatt 840
actatcgcca tctcgctcat catcggtcg gccgacggcg cacaggccat cgagttctat 900
cgggccagtc aggagacgtt ttcgatggca ttgcagaatg aggacctggc ggccgtccgc 960
gcgctgctaa gtatggcctt gtatacaatg ttgcaacaa gcggtccgag cgtgtggcat 1020
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gccagcttgg tggagagga gatggctaaa cgggccttct ggagtctgta caatctggac 1140
cgactgatcg ccagcacgtt aggacgacct cttggcttag cggacgagga catcaccgtg 1200
gggttggcac gcgagttcaa cgaggactgg accgaggcgc ccgggtcgag tgccatgacc 1260
attccagtgc aggtggtgcg actacgtcgg atcttttcgc gcatctaccg atatctgtac 1320

```



```

aacaatcagc cccacccct ttcattccgaa gtcaccgcc a cgtgcgcc tttccgacag 1380
gagctggacg attggcgacg cgcggctccc gtataccctc ccgccctcct ctactccaca 1440
agctactacg actatctatt tgcgacgaca gtactgtctca tgtaccgacc gagtccacgg 1500
aaccgacgc cagatactct gagcattatc agctgtggcg acgcgagcat ccaggtgatt 1560
cggtcgtact gggacagcta ctcggtaggc aaattgaagt ggatctgggt gacactgagc 1620
cagatctact tcgccggcat cagatcctg tgggtgtctgc atcagaactt gcgcgcgata 1680
caggacggtc aagcgccacc ctggcaaccg gatgaccaga ccatgcgccg ggggatccaa 1740
gcggttgctg tcctgatgga ggagtttggc aaacggcggc cgggggtgga acgtctggcg 1800
gagacattcc gtcaacaaag cagcagatc ttcagccatc tgggtggcata tcagcccaaa 1860
cctccaccgc agagccaacc cccggcacct ccaccattat cgcagtcaca atcgcagccc 1920
catatgctgg tggcgccgcc ggtcccgtg gccccgggtg tggacgacgt gctgctggtg 1980
gacgggtcag gcaatattcc cgtgatggat ccgtccatgg ccgaacaatt gttctattcg 2040
tacgattggt ttcaggagga gatggcgacg ttttataccc tc 2082

```

<210> 22

<211> 694

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 22

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Met Thr His Arg Asp Ser Asp Phe Arg His Gln Leu Gly Lys Phe Arg
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Leu Asp Thr Leu Pro Ser Pro Ala Val Ala Ala Ala Ala Pro Pro
      20          25          30
Leu Ile Ser Ser Thr Ser Ile Leu Ser Ser Pro Asn Thr Thr Thr
      35          40          45
Thr Thr Thr Thr Thr Thr Ser Ser Ser Gly Pro Val Arg Ser Lys Arg
      50          55          60
Val Ser Thr Ala Cys Asp Phe Cys Arg Lys Arg Lys Lys Lys Cys Asp
      65          70          75          80
Phe Arg Tyr Pro Asn Cys Ser Ala Cys Thr Arg Ala Gly Val Arg Cys
      85          90          95
Thr Ile Pro Pro Pro Gly Pro Gln Val Ala Ser Ala Ser Val Pro Arg
      100          105          110
Asp Gln Leu Glu Thr Leu Gln Asn Arg Val Arg Trp Leu Glu Asp Val
      115          120          125
Val Arg Arg Lys Thr Gly Ile Ser Val Ala Asp Arg Pro Thr Gly Thr
      130          135          140
Pro Leu Asp Gly Glu Gly Asp Pro Asp Trp Trp Tyr Gln Val Pro Ala
      145          150          155          160
Leu Met Met Thr Arg Asp Asn Leu Ser Arg Thr Ala Pro Gly Thr Thr
      165          170          175
Ala Gly Gly Val Thr Ser Ser Pro Ser Thr Ser Ser Pro Ser Ala Val
      180          185          190
Gly Pro Glu Leu Pro Asn Val Gly Glu Ile Phe Arg Asp Gln Leu Glu
      195          200          205
His Arg Arg Pro Ser Val Ala Arg Pro Val Ala Ser Ala Pro Arg Val
      210          215          220
Leu Arg Leu Ala Ser Leu Ala Glu Ala Glu Arg Val Ala Ala Gln Tyr
      225          230          235          240
Phe Asp Ser Met Gly Tyr Gln Tyr Pro Phe Leu His Arg Gly Asp Phe
      245          250          255
Leu Ala Gln Leu Arg Ser Leu Tyr Thr Ser Asp Ser Val Val Ala Pro
      260          265          270

```

Glu Val His Tyr Thr Tyr His Ile Thr Ile Ala Ile Ser Leu Ile Ile  
 275 280 285  
 Gly Ser Ala Asp Gly Ala Gln Ala Ile Glu Phe Tyr Arg Ala Ser Gln  
 290 295 300  
 Glu Thr Phe Ser Met Ala Leu Gln Asn Glu Asp Leu Ala Ala Val Arg  
 305 310 315 320  
 Ala Leu Leu Ser Met Ala Leu Tyr Thr Met Phe Ala Thr Ser Gly Pro  
 325 330 335  
 Ser Val Trp His Val Leu Gly Thr Ala Leu Arg Leu Ala Thr Ser Leu  
 340 345 350  
 Gly Leu His Lys Ala Arg Pro Ala Ala Ser Leu Val Glu Glu Glu Met  
 355 360 365  
 Ala Lys Arg Ala Phe Trp Ser Leu Tyr Asn Leu Asp Arg Leu Ile Ala  
 370 375 380  
 Ser Thr Leu Gly Arg Pro Leu Gly Leu Ala Asp Glu Asp Ile Thr Val  
 385 390 395 400  
 Gly Leu Pro Arg Glu Phe Asn Glu Asp Trp Thr Glu Ala Pro Gly Ser  
 405 410 415  
 Ser Ala Met Thr Ile Pro Val Gln Val Val Arg Leu Arg Arg Ile Phe  
 420 425 430  
 Ser Arg Ile Tyr Arg Tyr Leu Tyr Asn Asn Gln Pro Pro Pro Leu Ser  
 435 440 445  
 Ser Glu Val Thr Ala Thr Leu Arg His Phe Arg Gln Glu Leu Asp Asp  
 450 455 460  
 Trp Arg Arg Ala Ala Pro Val Tyr Pro Pro Ala Leu Leu Tyr Ser Thr  
 465 470 475 480  
 Ser Tyr Tyr Asp Tyr Leu Phe Ala Thr Thr Val Leu Leu Met Tyr Arg  
 485 490 495  
 Pro Ser Pro Arg Asn Pro Thr Pro Asp Thr Leu Ser Ile Ile Ser Cys  
 500 505 510  
 Gly Asp Ala Ser Ile Gln Val Ile Arg Ser Tyr Trp Asp Ser Tyr Ser  
 515 520 525  
 Val Gly Lys Leu Lys Trp Ile Trp Leu Thr Leu Ser Gln Ile Tyr Phe  
 530 535 540  
 Ala Gly Ile Thr Ile Leu Trp Cys Leu His Gln Asn Leu Arg Ala Ile  
 545 550 555 560  
 Gln Asp Gly Gln Ala Pro Pro Trp Gln Pro Asp Asp Gln Thr Met Arg  
 565 570 575  
 Arg Gly Ile Gln Ala Val Val Val Leu Met Glu Glu Phe Gly Lys Arg  
 580 585 590  
 Arg Pro Gly Val Glu Arg Leu Ala Glu Thr Phe Arg Gln Gln Ser Thr  
 595 600 605  
 Thr Ile Phe Ser His Leu Val Ala Tyr Gln Pro Gln Pro Pro Pro Gln  
 610 615 620  
 Ser Gln Pro Pro Ala Pro Pro Pro Leu Ser Gln Ser Gln Ser Gln Pro  
 625 630 635 640  
 His Met Leu Val Ala Pro Pro Val Pro Leu Ala Pro Val Leu Asp Asp  
 645 650 655  
 Val Leu Leu Val Asp Gly Ser Gly Asn Ile Pro Val Met Asp Pro Ser  
 660 665 670  
 Met Ala Glu Gln Leu Phe Tyr Ser Tyr Asp Trp Phe Gln Glu Glu Met  
 675 680 685  
 Ala Thr Phe Tyr Thr Leu  
 690

&lt;210&gt; 23

&lt;211&gt; 1371

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 23

```

atgtcgccca ctctgcaccc ccaggccttc tacggcacgt tgatccattc actcaaccca 60
tcgacaatcg aatacctccc caacacattg atcataatcg accaacaatgg aaaaatagag 120
ggactccatc cgcaaatccc cgcacacctc atccaatctc tcctggccac gcacaaccac 180
actaccacca gctgccaac caccatcctt tcgcccgcg agttcctcat tcccggattc 240
atcgacaccc acattcacgc tccccaatgg agtcaacgcg gcgtggggcg gggcatccca 300
ctgctcaact ggctggaggg gatcacgttc gcgcatgaag cgcgctgcag cgacgacgcc 360
tacgcgcggc ggctcttcca ctgctgcgtg agcggcggcc tcaaacaagg cgtcacgaca 420
gcctgctact acagttcgcg gcacgcctcg gcaacggtca tcctggccga gacgtgtctc 480
gcgctgggac agcgcgccct gctgggcaaa tgcaacatgg accggcacgc ggtcgactgg 540
tacgtcgacg agtcggcggc ggccctcggtc tccgacacgg agcacgtcat cggggcggtg 600
cgcgcgctgg acgccgagca cggcctcgtc acaccggtga tcacgccgcg gttcgcgac 660
agctgctcgg acgggctgct ccgggcgctg ggcgagctcg cggcgcgggc cgagtaccgc 720
gcgctgccca tccagacgca cttcaacgag tcgcggcagg agatggcgtt cacgcgcagc 780
ctgttccccg ggggtgcagga cgagacggcg ctgtacgagt cgtttgggct gctcaactcg 840
cggtgcggtg tggcgcatgc gatctacctg tcgcccgggg agatggaccg cgtgcaggcg 900
ctggactgtg ggatcgcgca ttgtcccgtg ccgaatacta ccatggacga gttcatggtg 960
gcgcctgtgc gggagtatct ggcgcggggg atgaaggtgg gtctggggac ggactgtggg 1020
ggtgggtttt cgtcgtcgat gctggatgtc atgcgcattg cgtttatggt gagtgtggca 1080
cgggagacgc agacggacgg ccgcgacaag ccgctgtctc ttgcgagggg gttctatctg 1140
gcgacggcgg gcggggcgag ggtgtgtggg ctggcggaga aggttgggcg gtttgcggtg 1200
ggcatggagt ttgatgcggt gctggtgagg acgggcgatg aggtcgatgg ggtcatgacg 1260
ccagtggagg aggaggattc gctcgagacg gtgtttgaga agttcttgat gacgggggat 1320
gatcgcaaca tgggtgcgagt ttttgtcaag gggagggagg tgaggggggt g 1371

```

&lt;210&gt; 24

&lt;211&gt; 457

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 24

```

Met Ser Pro Thr Leu His Pro Gln Ala Phe Tyr Gly Thr Leu Ile His
 1           5           10          15
Ser Leu Asn Pro Ser Thr Ile Glu Tyr Leu Pro Asn Thr Leu Ile Ile
          20          25          30
Ile Asp Gln His Gly Lys Ile Glu Gly Leu His Pro Gln Ile Pro Ala
          35          40          45
Ser Ser Ile Gln Ser Leu Leu Ala Thr His Asn His Thr Thr Thr Ser
          50          55          60
Cys Pro Thr Thr Ile Leu Ser Pro Ala Glu Phe Leu Ile Pro Gly Phe
          65          70          75          80
Ile Asp Thr His Ile His Ala Pro Gln Trp Ser Gln Arg Gly Val Gly
          85          90          95
Arg Gly Ile Pro Leu Leu Asn Trp Leu Glu Gly Ile Thr Phe Ala His
          100         105         110
Glu Ala Arg Cys Ser Asp Asp Ala Tyr Ala Arg Arg Leu Phe His Ser
          115         120         125

```

Cys Val Ser Gly Gly Leu Lys Gln Gly Val Thr Thr Ala Cys Tyr Tyr  
 130 135 140  
 Ser Ser Arg His Ala Ser Ala Thr Val Ile Leu Ala Glu Thr Cys Leu  
 145 150 155 160  
 Ala Leu Gly Gln Arg Ala Leu Leu Gly Lys Cys Asn Met Asp Arg His  
 165 170 175  
 Ala Val Asp Trp Tyr Val Asp Glu Ser Ala Ala Ala Ser Val Ser Asp  
 180 185 190  
 Thr Glu His Val Ile Arg Ala Val Arg Ala Leu Asp Ala Glu His Gly  
 195 200 205  
 Leu Val Thr Pro Val Ile Thr Pro Arg Phe Ala Ile Ser Cys Ser Asp  
 210 215 220  
 Gly Leu Leu Arg Ala Leu Gly Glu Leu Ala Ala Arg Ala Glu Tyr Arg  
 225 230 235 240  
 Ala Leu Pro Ile Gln Thr His Phe Asn Glu Ser Arg Gln Glu Met Ala  
 245 250 255  
 Phe Thr Arg Ser Leu Phe Pro Gly Val Gln Asp Glu Thr Ala Leu Tyr  
 260 265 270  
 Glu Ser Phe Gly Leu Leu Asn Ser Arg Cys Val Leu Ala His Ala Ile  
 275 280 285  
 Tyr Leu Ser Pro Arg Glu Met Asp Arg Val Gln Ala Leu Asp Cys Gly  
 290 295 300  
 Ile Ala His Cys Pro Val Pro Asn Thr Thr Met Asp Glu Phe Met Val  
 305 310 315 320  
 Ala Pro Val Arg Glu Tyr Leu Ala Arg Gly Met Lys Val Gly Leu Gly  
 325 330 335  
 Thr Asp Cys Gly Gly Phe Ser Ser Ser Met Leu Asp Val Met Arg  
 340 345 350  
 Met Ala Phe Met Val Ser Val Ala Arg Glu Thr Gln Thr Asp Gly Arg  
 355 360 365  
 Asp Lys Pro Leu Ser Leu Ala Glu Gly Phe Tyr Leu Ala Thr Ala Gly  
 370 375 380  
 Gly Ala Arg Val Cys Gly Leu Ala Glu Lys Val Gly Arg Phe Ala Val  
 385 390 395 400  
 Gly Met Glu Phe Asp Ala Val Leu Val Arg Thr Gly Asp Glu Val Asp  
 405 410 415  
 Gly Val Met Thr Pro Val Glu Glu Glu Asp Ser Leu Glu Thr Val Phe  
 420 425 430  
 Glu Lys Phe Leu Met Thr Gly Asp Asp Arg Asn Met Val Arg Val Phe  
 435 440 445  
 Val Lys Gly Arg Glu Val Arg Gly Leu  
 450 455

&lt;210&gt; 25

&lt;211&gt; 2832

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 25

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 atgaagcgac cgccccgcc ttttgtccag accgggggtca atggagtcaa ggctcagcaa 120  
 tcctcactct ccccgcaatc cgcgtcgaag cgtctccgg gcgcggcca aacttcttcg 180  
 gctacctcga tggctggaac caccgcaaat ggcatcaatg gcacgacaga cgcaagggt 240

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ccccgaatc gtccgaagag ggatgcgccg aagccagggg aggctgctgg ccggttacaa 300
aagctgcagt cgcgaccac gtccacggat ttgggcccagc gctccagcaa acaatgcgca 360
gaaccctatg tgaaaacgac aaattacatc ctcaagaaat actccaaatg tcctccatcg 420
cttgctctcc accttcaccc cacacatttc cgcttcgaac aacaagatgg gagttttccg 480
tataactccg aaatgaaggt tgtcatcgaa catcttcgcg ccggcactgt gcctcacgag 540
ataatagaag agctcctgcg tgccaacatc cggttctatg aaggctgtct catcgtacgg 600
gtgattgacc acaagtctgt gtccgcgcag gcgcgaaaga cgacagcaca ttcaccaat 660
gaaaataaca ccccttctc gatccacaac tataacgaac acataacacc atctgcctat 720
gtcccgtatc ctaaacagaa tcaattaacc tccgagaaag acgacacgaa ttctacagct 780
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cctctccata tggatcctcc accgtcgccg aagagaagga agcgacaggt ggcagagctt 1260
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cccaccacac gtatgagcca cgccagccca ggtcgggtcaa cgatggctcc tacaccggtg 2040
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cagcagcaac aaatgttgat gcagcaaaga cagcaactcc tggcgagca aggacatctc 2160
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cagtaccac cgacctttt gcagcaatac catgctgggc tcgaacgaa cgctaaggcc 2700
tgggtgagcg atatcatccg ccgagagcgt gaggccgcac agcaacaacg agcgaaccag 2760
gtcgtgccg tgcaagcgca agtcttgcat cagcaacagc agcagaacat gatgcagaac 2820
ggcatgggca aa 2832

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<210> 26

<211> 944

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 26

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His Pro Pro Lys Met Lys Arg Pro Pro Pro Pro Phe Val Gln Thr Gly

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Val	Asn	Gly	Val	Lys	Ala	Gln	Gln	Ser	Ser	Ser	Ser	Pro	Gln	Ser	Ala													
										35						40						45						
Ser	Lys	Arg	Leu	Pro	Gly	Ala	Gly	Gln	Thr	Ser	Ser	Ala	Thr	Ser	Met													
										50						55						60						
Ala	Gly	Thr	Thr	Ala	Asn	Gly	Ile	Asn	Gly	Thr	Thr	Asp	Ala	Lys	Gly													
65											70						75						80					
Pro	Leu	Asn	Arg	Pro	Lys	Arg	Asp	Ala	Pro	Lys	Pro	Gly	Glu	Ala	Ala													
										85						90						95						
Gly	Arg	Leu	Gln	Lys	Leu	Gln	Ser	Arg	Thr	Thr	Ser	Thr	Asp	Leu	Gly													
										100						105						110						
Gln	Arg	Ser	Ser	Lys	Gln	Cys	Ala	Glu	Pro	Tyr	Val	Lys	Thr	Thr	Asn													
										115						120						125						
Tyr	Ile	Leu	Lys	Lys	Tyr	Ser	Lys	Cys	Pro	Pro	Ser	Leu	Val	Leu	His													
130											135						140											
Leu	His	Pro	Thr	His	Phe	Arg	Phe	Glu	Gln	Gln	Asp	Gly	Ser	Phe	Pro													
145											150						155						160					
Tyr	Asn	Ser	Glu	Met	Lys	Val	Val	Ile	Glu	His	Leu	Arg	Ala	Gly	Thr													
										165						170						175						
Val	Pro	His	Glu	Ile	Ile	Glu	Glu	Leu	Leu	Arg	Ala	Asn	Ile	Arg	Phe													
										180						185						190						
Tyr	Glu	Gly	Cys	Leu	Ile	Val	Arg	Val	Ile	Asp	His	Lys	Ser	Val	Ser													
										195						200						205						
Ala	Gln	Ala	Arg	Lys	Thr	Thr	Ala	His	Ser	Ser	Asn	Glu	Asn	Asn	Thr													
										210						215						220						
Pro	Phe	Ser	Ile	His	Asn	Tyr	Asn	Glu	His	Ile	Thr	Pro	Ser	Ala	Tyr													
225											230						235						240					
Val	Pro	Tyr	Pro	Lys	Gln	Asn	Gln	Leu	Thr	Ser	Glu	Lys	Asp	Asp	Thr													
										245						250						255						
Asn	Ser	Thr	Ala	Gly	Asn	Gln	Ala	Asp	Ala	Pro	Asn	Gly	Glu	Gln	Ser													
										260						265						270						
Ala	Ser	Ala	Lys	Asp	Gln	Gly	Asp	Ser	Gly	Ser	Ser	Gln	Gln	Asn	Glu													
										275						280						285						
Ala	Pro	Ser	Lys	Pro	Arg	Val	Phe	Thr	Thr	Val	Leu	His	Pro	Thr	Pro													
										290						295						300						
Arg	Ser	Leu	Gln	Ala	Glu	Leu	Thr	Leu	Leu	Ala	Thr	Thr	Pro	Ala	Arg													
305											310						315						320					
Thr	Ser	Pro	Ala	Asn	Ser	Thr	Thr	Arg	Thr	Gln	Gly	Ala	Ser	Met	Ala													
										325						330						335						
Pro	Pro	Ser	Pro	Gly	Gly	Ser	Asn	Thr	Gln	Leu	Asp	Arg	Gly	His	Val													
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Ala	Lys	Lys	Gln	Lys	Met	Met	Val	Glu	Pro	Ala	Asp	Leu	Pro	Glu	Cys													
										355						360						365						
Glu	Ser	Arg	Leu	Thr	Arg	Ala	Leu	Ala	Pro	Pro	Leu	Phe	Leu	Asp	Pro													
										370						375						380						
Val	Asp	Ser	Phe	Asp	Ala	Ala	Gln	Asp	Leu	Leu	Arg	His	Met	Glu	Ser													
385											390						395						400					
Pro	Leu	His	Met	Asp	Pro	Pro	Pro	Ser	Pro	Lys	Arg	Arg	Lys	Arg	Thr													
										405						410						415						
Val	Ala	Glu	Leu	Ala	Ala	Asp	Glu	Ala	Leu	Ala	Ala	Glu	Glu	Glu	Arg													
										420						425						430						
Phe	Met	Leu	Ile	Met	Asp	Glu	Arg	Leu	Glu	Pro	Asn	Gly	Pro	Gly	Gly													
										435						440						445						
Ala	Gly	Gly	Pro	Lys	Ala	Ala	Ala	Val	Asp	Asp	Thr	Gly	Gly	Gly	Ala													
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Pro	Phe	Glu	Pro	Arg	Phe	Ser	Arg	Phe	Lys	Thr	Leu	Glu	Asn	Ile	Arg													
465											470						475						480					

```

Met Gln His Glu Glu Lys Ala Lys Arg Glu His Glu Ile Lys Leu Lys
      485      490      495
Gln Glu Leu Ala Lys Arg Gln Gln Gln Glu Gln Glu Arg Glu Arg Arg
      500      505      510
Arg Ala Leu Glu Gln Arg Gln Ala Glu Glu His Ala Lys Asp Glu Ala
      515      520      525
Arg Arg Gln His Leu Ala Ala Gln Gln Gln Ala Gln Ala Gln Leu Ala
      530      535      540
Ala Gln Gln Gln Asn Arg His Val Met Ala Gln Ala Asn Gly Val Ser
545      550      555      560
Gln Ala Pro Gln Ser Ser Pro Val Val Arg Asn Gln Thr Pro His Asn
      565      570      575
Thr Ser Ser Pro Leu Val Gly Asn Ala Met Gly Thr Gln Ala Gly Val
      580      585      590
Pro Met Ser Met Thr Ser Ser Met Gln Gly Ala Gly Ser Pro Gln Arg
      595      600      605
Pro Pro Ser Ala Leu Gln His Ala His Pro Asn Leu Met Ser His Pro
      610      615      620
Met Ala Ala Ser Arg Ser Gln Gln Gly Pro Ser Arg His Gly Thr Pro
625      630      635      640
Gln Met Thr Gln Gly Thr Pro Ala Met Ser His Ala Thr Pro Ile Met
      645      650      655
Arg Asn Val Thr Pro Thr Gln Arg Met Ser His Ala Ser Pro Gly Arg
      660      665      670
Ser Thr Met Ala Pro Thr Pro Val Met Asn Gln Ala Met Met Gly Thr
      675      680      685
Pro Gln Met Ala Gly Gly Met Gly Leu Thr Pro Gln Gln Gln Gln
      690      695      700
Met Leu Met Gln Gln Arg Gln Gln Leu Leu Ala Gln Gln Gly His Leu
705      710      715      720
Gly His Gly Gln Leu Thr Pro Gln Gln Tyr Ala Gln Leu Gln Ala Asn
      725      730      735
Ala His Ala Gln Gln Ser Ile Gln Ser His Pro Gln His Met Met Gln
      740      745      750
Ala Gln Gln Gln Asn Gln Gln Gln Pro Lys Ile Pro Asn Gln Gln Ala
      755      760      765
Tyr Gln Ser Gln Met Met Arg Ala Gln Leu Ala Gln Leu Gln Met Val
      770      775      780
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
785      790      795      800
Gln Gln Ser Gln Gly Gln Gln Ala His Val His Gln Gly Ser Pro Gln
      805      810      815
Met Asn Pro Gln Gln Gln Met Met Met Ala Ala Ala Gln Ala Asn Ser
      820      825      830
Gly His Pro Pro Gln Asn Met Gln Gly Val Ser Met Ala Gln Gly Ala
      835      840      845
Met Ala Gln Arg Tyr Asn Asn Met Tyr Gln Gln Arg Leu Leu Arg Leu
      850      855      860
Arg Gln Glu Met Ala Ser Lys Leu Met Pro Gln Tyr Gly Pro Pro Gly
865      870      875      880
Gln Tyr Pro Pro His Leu Leu Gln Gln Tyr His Ala Gly Leu Glu Arg
      885      890      895
Asn Ala Lys Ala Trp Val Ser Asp Ile Ile Arg Arg Glu Arg Glu Ala
      900      905      910
Ala Gln Gln Gln Arg Ala Asn Gln Val Ala Ala Val Gln Ala Gln Val
      915      920      925
Leu Gln Gln Gln Gln Gln Gln Asn Met Met Gln Asn Gly Met Gly Lys

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930

935

940

<210> 27  
 <211> 2043  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 27  
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 tatctctacc aacatccgcc gttcgacatg gtcgacttct accccatcat ggactacgag 180  
 gaatacgcag agaacctgtc ccgtccgata ttgaccaaag aacaagtcca gactctcgag 240  
 gcccaattcc aggtcatccc gaagcccagt agcaacgtca agcgccaatt ggccgctcaa 300  
 acaaatctca gtcttccccg agtcgcgaac tggttccaaa acagacgggc caaagcgaag 360  
 cagcagaaac gtcaggaaga attcgagcgc atgcagaagg cgaaagcgga ggccgaggaa 420  
 gccgcccggg gcaaatcaga gaacgaaccc aacgcggaat ccacctcgga ctccaaacct 480  
 tccacagaca acaagaccga caaggtcacg cctcagcaat cttccagcac ggacacgacg 540  
 gaggaccaat ccaagaccgc ggcgtctgca tcgtccagtc gatccaagca caagaaaaca 600  
 cgcagtgaat ccgctcgcga ggccactttt gcttcgctgc aacgagcgtt gaacgcgcgc 660  
 gttgcagctc gcgaccacaa tagccctgac aatgaacatc gtccagctgg aaatcccaac 720  
 gccgaggggt ccatctcccc cgcaaccccc ttctctgaca cacacactcc gggtcaccat 780  
 tacgcccagc tccagagtgc ccagagtgcg ctcaataccc cctatccga gtgggatcac 840  
 tcgaagcatt gggctccgtc tcagagtcc tgcagaatct ttggctcaca acatactcac 900  
 aatgtcatgc cgagcgtaca attccctca tcacagagtg aagaatgggc tggccaagta 960  
 cagccaacgg acaactcatt ccacacgatg cagtatcctg tacagccgga gatggcactt 1020  
 tcgaagcgag gctcatcgga agagctggca agcacgcttg aaggcatcgg catccacacc 1080  
 accgggtcga acggcctgtc acacctctcc acgggaccgg agcgtccac ctggagggaa 1140  
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 acttccagat ctctctcgat gctcgcggga tcgtcttcca tgtctccac gacaagagt 1260  
 ccgagctatg gcgccagtca cggagtgaga cagtcgaagt caacacaatg cctcaactcc 1320  
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 ctcccgaata ctcccaccga tgggggatac tgcctgtcag cccaaccgac gagtgggttg 1560  
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 ccgcagcagg cggatgggtc tatgtcgtat gagcgtctgt tcgacacggt ccctatctca 1860  
 gagtctccct ctttgggtga ttcaactagc gagggcgacc tgtcgggtga cgctgactcc 1920  
 aaaggcatgg agttctgcat ccaggaattc cctgaacagc aagaagctca tcgattcgtt 1980  
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 ttc 2043

<210> 28  
 <211> 681  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 28



```

Met Asn Tyr Leu His Gln Pro Tyr Gln Tyr Val Ala His Pro Gly Ile
 1      5      10      15
Pro Met Asp Gln Pro Met Ser Phe Asp Pro Thr Met Gly His Pro Ala
 20      25      30
Met Met His Pro Met Asp Gly Gly Tyr Leu Tyr Gln His Pro Pro Phe
 35      40      45
Asp Met Val Asp Phe Tyr Pro Ile Met Asp Tyr Glu Glu Tyr Ala Glu
 50      55      60
Asn Leu Ser Arg Pro Ile Leu Thr Lys Glu Gln Val Glu Thr Leu Glu
 65      70      75      80
Ala Gln Phe Gln Ala His Pro Lys Pro Ser Ser Asn Val Lys Arg Gln
 85      90      95
Leu Ala Ala Gln Thr Asn Leu Ser Leu Pro Arg Val Ala Asn Trp Phe
100      105      110
Gln Asn Arg Arg Ala Lys Ala Lys Gln Gln Lys Arg Gln Glu Glu Phe
115      120      125
Glu Arg Met Gln Lys Ala Lys Ala Glu Ala Glu Glu Ala Ala Arg Gly
130      135      140
Lys Ser Glu Asn Glu Pro Asn Ala Glu Ser Thr Ser Asp Ser Lys Pro
145      150      155      160
Ser Thr Asp Asn Lys Thr Asp Lys Val Thr Pro Gln Gln Ser Ser Ser
165      170      175
Thr Asp Thr Thr Glu Asp Gln Ser Lys Thr Ala Ala Ser Ala Ser Ser
180      185      190
Ser Arg Ser Lys His Lys Lys Thr Arg Ser Glu Ser Ala Arg Glu Ala
195      200      205
Thr Phe Ala Ser Leu Gln Arg Ala Leu Asn Ala Ala Val Ala Ala Arg
210      215      220
Asp His Asn Ser Pro Asp Asn Glu His Arg Pro Ala Gly Asn Pro Asn
225      230      235      240
Ala Glu Gly Ser Ile Ser Pro Ala Thr Pro Phe Leu Asp Thr His Thr
245      250      255
Pro Gly His His Tyr Ala Asp Val Gln Ser Ala Gln Ser Ala Leu Asn
260      265      270
Thr Pro Tyr Pro Glu Trp Asp His Ser Lys His Trp Ala Pro Ser Gln
275      280      285
Ser Pro Ala Glu Ser Leu Gly Ser Gln His Thr His Asn Val Met Pro
290      295      300
Ser Val Gln Phe Pro Ser Ser Gln Ser Glu Glu Trp Ala Gly Gln Val
305      310      315      320
Gln Pro Thr Asp Asn Ser Phe His Thr Met Gln Tyr Pro Val Gln Pro
325      330      335
Glu Met Ala Leu Ser Lys Arg Gly Ser Ser Glu Glu Leu Ala Ser Thr
340      345      350
Leu Glu Gly Ile Gly Ile His Thr Thr Gly Ser Asn Gly Leu Ser His
355      360      365
Leu Ser Thr Gly Pro Glu Arg Pro Thr Trp Arg Glu Thr Gly Lys Glu
370      375      380
Leu Asp Leu Ala Ala Arg Arg Lys Arg Pro Arg Pro Ala Ala Ile Gly
385      390      395      400
Thr Ser Arg Ser Ser Ser Met Leu Ala Gly Ser Ser Ser Met Ser Pro
405      410      415
Thr Thr Arg Val Pro Ser Tyr Gly Ala Ser His Gly Val Arg Gln Ser
420      425      430
Lys Ser Thr Gln Cys Leu Asn Ser Arg Tyr Ala Gly Val Arg Lys Ala
435      440      445
Ser Ala Ala Gln Arg Ser Pro Leu Asn Leu Ser Asn Phe Ala Glu Ala

```

450		455		460											
Gly	Ala	Phe	Gly	Ser	Lys	Ala	Glu	Met	Ser	Ser	Met	Leu	Gln	Pro	Ala
465					470					475					480
Val	Thr	Thr	Gly	Ala	Leu	Ala	Pro	Pro	Thr	Pro	Leu	Thr	Pro	Glu	Asp
			485						490					495	
Leu	His	His	Leu	Leu	Pro	Asn	Thr	Pro	Thr	Asp	Gly	Gly	Tyr	Cys	Leu
			500					505					510		
Ser	Ala	Gln	Pro	Thr	Ser	Gly	Leu	Phe	Pro	Thr	Thr	Gln	Pro	Met	Gln
		515					520					525			
Ile	Asn	Ile	Ala	Ser	Pro	Pro	Ala	Thr	Pro	Leu	Gly	Val	Asp	Leu	Met
	530					535					540				
Ser	Ser	Tyr	Pro	Tyr	Asn	Asn	Val	Ala	Pro	Pro	Met	Ser	Ala	Pro	Ala
545					550					555					560
His	Tyr	Thr	Ser	Phe	Pro	Glu	Tyr	Val	His	Cys	Asp	Ser	Ala	Thr	Met
			565						570					575	
Thr	Gly	Arg	Ser	Trp	Thr	Asp	Ala	Thr	Ser	Met	Pro	Ser	Pro	Glu	Ala
			580					585					590		
Ser	Phe	Gln	Ser	Arg	Cys	Pro	Met	Pro	Gln	Gln	Ala	Asp	Gly	Ser	Met
	595					600						605			
Ser	Tyr	Glu	Arg	Ser	Val	Asp	Thr	Val	Pro	Ile	Ser	Glu	Ser	Pro	Ser
	610					615					620				
Leu	Val	Tyr	Ser	Thr	Ser	Glu	Gly	Asp	Leu	Ser	Val	His	Ala	Asp	Ser
625					630					635					640
Lys	Gly	Met	Glu	Phe	Cys	Ile	Gln	Glu	Phe	Pro	Glu	Gln	Gln	Glu	Ala
			645						650					655	
His	Arg	Phe	Val	Ala	Gln	Gln	Met	Ser	Gln	Lys	Pro	Lys	Ala	Tyr	Thr
		660						665					670		
Phe	Asn	Asn	Gln	Thr	Pro	Asn	Asp	Phe							
	675					680									

<210> 29  
 <211> 792  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 29  
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 cagcagcaac aaatgttgat gcagcaaaga cagcaactcc tggcgagca aggacatctc 120  
 ggtcatggcc agcttactcc gcaacagtac gctcagttgc aagcgaatgc tcatgcacag 180  
 cagagtatcc agtcgcaccc acagcacatg atgcaagcgc aacagcagaa ccagcaacag 240  
 ccaaagatac cgaatcaaca ggcctatcaa agccagatga tgcgtgcgca gctcgcgag 300  
 ttgcagatgg tccagcaaca acaacagcag cagcagcagc agcagcagca acagcaacag 360  
 caacagtccc agggccagca ggctcatgta caccagggca gtccgcagat gaaccccaa 420  
 cagcagatga tgatggcagc cgcccaagcc aacagcggac atccaccgca gaacatgcag 480  
 ggagtaagca tggcacaagg tgctatggcg cagcgctaca ataacatgta ccaacagcgc 540  
 ttgctacggt tgaggcaaga aatggcgctc aagttgatgc ccagtacgg gcccccgggg 600  
 cagtaccac cgacactttt gcagcaatac catgctgggc tcgaacggaa cgctaaggcc 660  
 tgggtgagcg atatcatccg ccgagagcgt gaggccgcac agcaacaacg agcgaaccag 720  
 gtcgctgccg tgcaagcgca agtcttgag cagcaacagc agcagaacat gatgcagaac 780  
 ggcattggca aa 792

<210> 30  
 <211> 264

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 30

```

Met Asn Gln Ala Met Met Gly Thr Pro Gln Met Ala Gly Gly Met Gly
 1          5          10          15
Leu Thr Pro Gln Gln Gln Gln Gln Met Leu Met Gln Gln Arg Gln Gln
 20          25          30
Leu Leu Ala Gln Gln Gly His Leu Gly His Gly Gln Leu Thr Pro Gln
 35          40          45
Gln Tyr Ala Gln Leu Gln Ala Asn Ala His Ala Gln Gln Ser Ile Gln
 50          55          60
Ser His Pro Gln His Met Met Gln Ala Gln Gln Gln Asn Gln Gln Gln
 65          70          75          80
Pro Lys Ile Pro Asn Gln Gln Ala Tyr Gln Ser Gln Met Met Arg Ala
 85          90          95
Gln Leu Ala Gln Leu Gln Met Val Gln Gln Gln Gln Gln Gln Gln
100          105          110
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Gln Gly Gln Gln Ala
115          120          125
His Val His Gln Gly Ser Pro Gln Met Asn Pro Gln Gln Gln Met Met
130          135          140
Met Ala Ala Ala Gln Ala Asn Ser Gly His Pro Pro Gln Asn Met Gln
145          150          155          160
Gly Val Ser Met Ala Gln Gly Ala Met Ala Gln Arg Tyr Asn Asn Met
165          170          175
Tyr Gln Gln Arg Leu Leu Arg Leu Arg Gln Glu Met Ala Ser Lys Leu
180          185          190
Met Pro Gln Tyr Gly Pro Pro Gly Gln Tyr Pro Pro His Leu Leu Gln
195          200          205
Gln Tyr His Ala Gly Leu Glu Arg Asn Ala Lys Ala Trp Val Ser Asp
210          215          220
Ile Ile Arg Arg Glu Arg Glu Ala Ala Gln Gln Gln Arg Ala Asn Gln
225          230          235          240
Val Ala Ala Val Gln Ala Gln Val Leu Gln Gln Gln Gln Gln Gln Asn
245          250          255
Met Met Gln Asn Gly Met Gly Lys
260

```

&lt;210&gt; 31

&lt;211&gt; 1290

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 31

```

atgccgccac cagcctctgc agtggatttc tcgaatctac tgaaccccca aggcaacgcc 60
acctcttcca ctcccttcgac tcccgtggac agctccaagg cgccgtccac tcctaccagt 120
gttcagtccta acacgagtat ggcctcatcg gtgagcctcc tcccacctct catgaaagga 180
gcgcgccccg ccaacgaaga agtccgccag gatcttcttc gcccttataa gtgccccctc 240
tgtgaccgtg ccttcaccg cttggaacac cagaccagac acatccgcac ccatacgggt 300

```

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gaaaagccgc acgcatgccg gtcccccgga tgcacgaagc gcttcagtcg ctccgatgag 360
ctgacgcgcc actcccggat ccacaacaac cccaactccc gacgcagtaa caaggcgcaa 420
catctggccg ccgctgctgc tgcgcgcgcc gcgggtcagg acaatgcgat ggtcggcgcc 480
ccggcagggg ccatgatgcc tctcccagc aagcccatca cgcggtccgc ccccgctctcg 540
caggtgggat ccccgacgt gtccccgctt cattcgtact ccaactacgc cggtcacatg 600
cggtcgaact tgggaccgta tgcccggcac ggcgagcggg cgtcttcggg catggatatc 660
aacctcctcg cgaccgctgc ctgcgaagtc gagcgcgatg agcactacgg cttccacggg 720
ccccgtggtc acccgttctt tgcgccccgt catcacggcg gcaccggtcg tctcccgtcg 780
ctgtcggcct acgcgatctc gcacagcatg agtcgctcgc attcccacga ggatgacgat 840
gcttacacgc agcatcgct gaagcgctcc cgcccact cccccaactc gaccgcccc 900
tctctccca ccttctcgca cgattcgctt tctcccacgc ccgaccacac tccgctggcg 960
accctgccc attcgccgcy gctgcgccct ctgggtgcca gtgaactgca tctgccttcg 1020
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ggcccact actacagccc tgcccagggt cacgtgggtc ccagcatcag cgacatcatg 1140
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caggacatgc tgaatccggc gacgggattt tcgtcgggtg cctcgtcgac gaacaactcc 1260
gtcgcggtg gcgatctggc agaccgtttc 1290

```

<210> 32

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 32

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Met Pro Pro Pro Ala Ser Ala Val Asp Phe Ser Asn Leu Leu Asn Pro
 1          5          10          15
Gln Gly Asn Ala Thr Ser Ser Thr Pro Ser Thr Pro Val Asp Ser Ser
          20          25          30
Lys Ala Pro Ser Thr Pro Thr Ser Ala Gln Ser Asn Thr Ser Met Ala
          35          40          45
Ser Ser Val Ser Leu Leu Pro Pro Leu Met Lys Gly Ala Arg Pro Ala
          50          55          60
Asn Glu Glu Val Arg Gln Asp Leu Pro Arg Pro Tyr Lys Cys Pro Leu
65          70          75          80
Cys Asp Arg Ala Phe His Arg Leu Glu His Gln Thr Arg His Ile Arg
          85          90          95
Thr His Thr Gly Glu Lys Pro His Ala Cys Gln Phe Pro Gly Cys Thr
          100          105          110
Lys Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ser Arg Ile His
          115          120          125
Asn Asn Pro Asn Ser Arg Arg Ser Asn Lys Ala Gln His Leu Ala Ala
          130          135          140
Ala Ala Ala Ala Ala Ala Ala Gly Gln Asp Asn Ala Met Val Gly Ala
145          150          155          160
Pro Ala Gly Ala Met Met Pro Pro Pro Ser Lys Pro Ile Thr Arg Ser
          165          170          175
Ala Pro Val Ser Gln Val Gly Ser Pro Asp Val Ser Pro Pro His Ser
          180          185          190
Tyr Ser Asn Tyr Ala Gly His Met Arg Ser Asn Leu Gly Pro Tyr Ala
          195          200          205
Arg His Gly Glu Arg Ala Ser Ser Gly Met Asp Ile Asn Leu Leu Ala
          210          215          220
Thr Ala Ala Ser Gln Val Glu Arg Asp Glu His Tyr Gly Phe His Gly
225          230          235          240

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Pro Arg Gly His Pro Phe Phe Ala Pro Arg His His Gly Gly Thr Gly
      245      250      255
Arg Leu Pro Ser Leu Ser Ala Tyr Ala Ile Ser His Ser Met Ser Arg
      260      265      270
Ser His Ser His Glu Asp Asp Asp Ala Tyr Thr Gln His Arg Val Lys
      275      280      285
Arg Ser Arg Pro Asn Ser Pro Asn Ser Thr Ala Pro Ser Ser Pro Thr
      290      295      300
Phe Ser His Asp Ser Leu Ser Pro Thr Pro Asp His Thr Pro Leu Ala
305      310      315      320
Thr Pro Ala His Ser Pro Arg Leu Arg Pro Leu Gly Ala Ser Glu Leu
      325      330      335
His Leu Pro Ser Ile Arg His Leu Ser Leu His His Thr Pro Ala Leu
      340      345      350
Ala Pro Met Glu Pro Gln Pro Glu Gly Pro Asn Tyr Tyr Ser Pro Ala
      355      360      365
Gln Gly His Val Gly Pro Ser Ile Ser Asp Ile Met Ser Arg Pro Asp
370      375      380
Gly Thr Gln Arg Lys Leu Pro Val Pro Gln Val Pro Lys Val Ala Val
385      390      395      400
Gln Asp Met Leu Asn Pro Ala Thr Gly Phe Ser Ser Val Ser Ser Ser
      405      410      415
Thr Asn Asn Ser Val Ala Gly Gly Asp Leu Ala Asp Arg Phe
      420      425      430

```

&lt;210&gt; 33

&lt;211&gt; 3645

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 33

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atgaatcccg caaacttcaa cgtggggcggc tccatgcccg ccgcgcccac ccccagatg 60
ccgagactcg acaataacca ggtcatgatg aactatgtcg ccagggttt acatgcacaa 120
ggcacctata ccggttgcg cgccgaagtg cccatgaaag agcgcgtggt tcgagtgtat 180
caaatgttca cctcccttcg ccttatccaa cccaagcag atctgcaaca cctggcccaa 240
gctgccctca gctttgagca gaaggccttc aaagacgctc agcagaaagt cgattacgac 300
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atgcagaatg gcatgattcc cccgggcgct cccaaagccg gcgcatgctg tggcgctcga 420
caaccctect tcccgcaaca gatgaatcga gccatgcaat ccaatcccat ggccggtcaa 480
caagccatgg ccatggggat gaccgatccg aatcaacagg ccgcatgcc gcagcgatcg 540
caacagcagc aagccatgat gcagcagcag cagcaacaac agcaacaaca gcaacagcag 600
cagcagcagc agcagccacg cgctcaacaa cgctccgcca ataccctcgc cctggctcgac 660
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aaccaacaac cgttcaacaa cgcccagaac accttccga tgggccaaca gctcgcgag 1200
ggaggacagg ctaatctggg cgctgccggc atcaaccccc agatgttcgc ccaacaacac 1260
atgcaaaaac ccccgaaat gcccgcggat cggccccagc cgcccgcccc tttccagccc 1320

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cagactcaag cacagaacca ggctcaggcc caggcccgcg cccaggcagc tcaaaaagcc 1380
cagatggcga tttcccaggc cggccaagct aattcgcacc tgcaacagcc catgccgcag 1440
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cctccgccga agaagagaaa gcagtcctcat ccaggggcta cccccaccgt cggcacgcct 3600
gctaccaagc cgccaaccac ccggcccgcg gacgtcaaaa tgccc 3645

```

<210> 34

<211> 1215

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 34

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Met Asn Pro Ala Asn Phe Asn Val Gly Gly Ser Met Pro Ala Ala Pro
 1           5           10           15
Thr Pro Gln Met Pro Arg Leu Asp Asn Asn Gln Val Met Met Asn Tyr
          20          25          30
Val Ala Gln Ala Leu His Ala Gln Gly Thr Tyr Thr Gly Trp Arg Ala
          35          40          45
Glu Val Pro Met Lys Glu Arg Val Val Arg Val Tyr Gln Met Phe Thr
          50          55          60

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Ser Leu Arg Leu Ile Gln Pro Gln Ala Asp Leu Gln His Leu Ala Gln
65      70      75      80
Ala Ala Leu Ser Phe Glu Gln Lys Ala Phe Lys Asp Ala Gln Gln Lys
85      90      95
Val Asp Tyr Asp Lys Glu Cys Asn Asp Lys Leu Leu His Ile Arg Asp
100     105     110
Thr Arg Ala Arg Gln Ala Ala Val Met Gln Asn Gly Met Ile Pro Pro
115     120     125
Gly Ala Pro Lys Ala Gly Gly Met Arg Gly Val Gly Gln Pro Ser Phe
130     135     140
Pro Gln Gln Met Asn Arg Ala Met Gln Ser Asn Pro Met Ala Gly Gln
145     150     155     160
Gln Ala Met Ala Met Gly Met Thr Asp Pro Asn Gln Gln Ala Ala Met
165     170     175
Pro Gln Arg Ser Gln Gln Gln Gln Ala Met Met Gln Gln Gln Gln Gln
180     185     190
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Arg Ala
195     200     205
Gln Gln Arg Ser Ala Asn Thr Leu Ala Leu Val Asp Glu Leu Asn Asn
210     215     220
Leu Thr Pro Gln Glu Tyr Glu Asn Val Asn Arg Val Ala His Gln Ile
225     230     235     240
Met Thr Lys Thr Ser Pro Val Asp Ala Glu Lys Ile Lys Arg Asn Leu
245     250     255
Gln Asn Met Asn Pro Val Gln Arg Arg Tyr Leu Thr Glu Arg Asn Ile
260     265     270
Asp Pro Val Ala Tyr Phe Phe Arg Ser Gln Ala Leu Ala His Leu Lys
275     280     285
Arg Gln Met Lys Ala Arg Val Asp Met Ser His Pro Gln Asn Thr Gly
290     295     300
Val Asp Pro Asn Asn Val Met Met Gly Ala Asp Pro Thr Met Asn Pro
305     310     315     320
Gln Met Phe Pro Asn Met Met Asn Leu Gln Arg Asn Ser Ala Phe Ala
325     330     335
Met Gly Asn Gln Pro Asn Met Asp Pro Ser Ser Phe Ile Gly Asn Val
340     345     350
Glu Asn Ile Gln Gly Gln Gln Ala Asp Gly Leu Arg Ser Gln Glu Ala
355     360     365
Gly Gln Leu Val Val Pro Ala Ser Ser Ser Gln Met Asn Gln Gln Pro
370     375     380
Phe Asn Asn Ala Gln Asn Thr Phe Pro Met Gly Gln Gln Leu Ala Gln
385     390     395     400
Gly Gly Gln Ala Asn Leu Gly Ala Ala Gly Ile Asn Pro Gln Met Phe
405     410     415
Ala Gln Gln His Met Gln Asn Thr Pro Asn Met Pro Pro Asp Arg Pro
420     425     430
Gln Pro Ala Ala Pro Phe Gln Pro Gln Thr Gln Ala Gln Asn Gln Ala
435     440     445
Gln Ala Gln Ala Arg Ala Gln Ala Ala Gln Lys Ala Gln Met Ala Ile
450     455     460
Ser Gln Ala Gly Gln Ala Asn Ser His Leu Gln Gln Pro Met Pro Gln
465     470     475     480
Gln Ser Pro Ala Met Pro Met Leu Asn Arg Pro Met Pro Pro Gly Gln
485     490     495
Met Ser Pro Ala Gln Met Ala Ala Gln Val Arg Pro Pro Ser Arg Ala
500     505     510
Pro Ala Met Gly Gln Gln Pro Ser Met Gly Gly Gln Gln Pro Met Gln

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515					520					525					
Gly	Arg	Pro	Gln	Ile	Pro	Pro	Gly	Leu	Pro	Pro	Ala	Ile	Gln	Glu	Gln
530							535				540				
Leu	Ala	Gln	Met	Ser	Pro	Glu	Gln	Leu	Asn	Arg	Val	Leu	Ala	Gln	Arg
545					550					555					560
Arg	Ala	Met	Ala	Asn	Asn	Pro	Ala	Leu	Ala	Arg	Ala	Asn	Ala	Ala	Arg
				565						570					575
Gln	Ser	Val	Pro	Met	Gln	Gln	Ser	Val	Ser	Gln	Ser	Ala	Gln	Ala	Gln
			580						585				590		
Ser	Met	Ala	Asn	Asn	Gln	Asn	Met	Arg	Ala	Met	Asn	Val	Gln	Ala	Gln
		595					600					605			
Leu	Ala	Gly	Met	Gly	Gly	Ala	Gln	Gln	Met	Met	Pro	Gly	Gln	Gln	Met
610						615					620				
Ser	Leu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Arg	Gln	Glu
625					630					635					640
Leu	Tyr	Lys	Met	Gln	Leu	Leu	Gln	Gln	Ser	Gly	Gly	Asn	Leu	Glu	Leu
				645					650						655
Ser	Asn	Glu	Gln	Ser	Lys	Glu	Met	Asp	Arg	Leu	His	Phe	Pro	Pro	Ser
			660					665					670		
Leu	Leu	Gly	Asn	Asn	Pro	Asn	Ile	Val	Ser	Leu	Val	Pro	Lys	Asn	Ile
		675					680					685			
Lys	Thr	Trp	Gly	Gln	Leu	Lys	Gln	Trp	Ala	Ala	Thr	Asn	Pro	Gln	Leu
690						695					700				
Pro	Gly	Gly	Leu	Asn	Leu	Gln	Lys	Leu	Met	Ala	Leu	Gln	Lys	Phe	His
705					710					715					720
Phe	Thr	Gln	Ile	Leu	Asn	Gln	Ser	Lys	Glu	Arg	Ser	Arg	Asn	Pro	Asp
				725					730					735	
Gln	Ala	Gly	Gln	Gly	Pro	Trp	Met	Ser	Gly	Pro	Thr	Gln	Ala	Pro	Gln
			740					745					750		
Gln	Pro	Pro	Met	Met	Asn	Pro	Gln	Gln	Phe	Pro	Pro	Gly	Gln	Gln	Gln
		755					760					765			
Ala	Ala	Ile	Asn	Met	Ala	Ala	Ile	Arg	Pro	Val	Thr	Ala	Gln	Asp	Ile
770						775					780				
Gln	Ala	Ala	Arg	Gln	Arg	His	Pro	Ala	Met	Ala	Gln	Asn	Phe	Thr	Asp
785					790					795					800
Asp	Gln	Ile	Arg	Glu	Ser	Leu	Asn	Lys	Ala	Arg	Gln	Arg	Gln	Leu	Met
				805					810					815	
Leu	Leu	Ala	Gln	Gln	Arg	Ala	Ala	Gln	Ala	Gln	Glu	Leu	Ala	Ala	Gln
			820					825					830		
Gln	Gln	Gln	Thr	Gln	Ala	Leu	Gln	Gln	Thr	Pro	Val	Gly	Gly	Pro	Ala
			835				840					845			
Pro	Gly	Pro	His	Leu	Arg	Pro	Glu	Gly	Pro	Gly	Gln	Pro	Ala	Thr	Gln
		850				855					860				
Pro	Gln	Gln	Gln	Ser	Pro	Ala	Thr	Lys	Ala	Pro	Ser	Thr	Val	Pro	Gly
865					870					875					880
Lys	Lys	Ala	Pro	Pro	Ala	Lys	Gln	Gln	Pro	Ala	Lys	Arg	Lys	Leu	Pro
				885					890					895	
Ser	Asp	Glu	Thr	Ala	Asp	Ala	Gln	Asn	Pro	Asp	Asn	Gln	Val	Ala	Gln
			900				905						910		
Lys	Pro	Thr	Gln	Ala	Gly	Ala	Pro	Gln	Gly	Val	Ala	Ala	Pro	Ala	Pro
			915				920					925			
Ser	Lys	Pro	Asn	Met	Pro	Phe	Thr	Arg	Glu	Gln	Leu	Ala	Ala	Met	Thr
930						935						940			
Pro	Gln	Gln	Arg	Ala	Gln	Ile	Glu	Ala	His	Met	Arg	Arg	Gln	Gln	Gly
945					950					955					960
Gln	Thr	Arg	Thr	Lys	Ala	Ala	Ala	Glu	Glu	Ala	Trp	Asn	Asn	Leu	Pro
				965					970						975



Glu Lys Ile Arg Gln Ala Tyr His Asp Thr Leu Lys Gln Ala Pro Pro  
 980 985 990  
 Met Lys Phe Ala Ala Ile Thr Pro Glu Gln His Ala Ala Met Asn Gln  
 995 1000 1005  
 Gln Leu Arg Asp Cys Thr Asp Met Leu Gly Arg Met Asp Thr Leu Val  
 1010 1015 1020  
 Gln Trp Phe Ala Lys Ile Pro Gly Gln Glu Lys Asn Val Arg Ser Leu  
 1025 1030 1035 1040  
 Leu Ala Met Arg Ile Gln Leu Met Arg Gln Phe Lys Asn Ser Pro Asp  
 1045 1050 1055  
 Trp Val Leu Asn Asp Ser Leu Thr Ile Ser Pro Glu Asn Leu Thr Ala  
 1060 1065 1070  
 Thr Ile Asn Tyr Ile Lys Lys Leu Phe His Ala Met Ile Thr Arg Val  
 1075 1080 1085  
 Ser Gln His Gln Asn Gln Ala Pro Gly Gln Arg Pro Gly Gly Pro Gln  
 1090 1095 1100  
 Pro Pro Leu Thr Gln Ala Ser Gln Asn Ala Met Pro Ala Leu Asn Ala  
 1105 1110 1115 1120  
 Thr Asn Leu Gln Gln Leu Gln Gln Glu Glu Ala Leu Gln Arg Ala  
 1125 1130 1135  
 Arg Arg Ala Ser Ser Gln Thr Ala Val Ser Ala Thr Ser Ala Val Pro  
 1140 1145 1150  
 Pro Ala Pro Phe Gly Ala Pro Ser Pro Gln Gly Val Pro His Ala Tyr  
 1155 1160 1165  
 Gly Pro Gly Ser Met Pro Pro Glu Gln Leu Lys Leu Pro Pro Pro Lys  
 1170 1175 1180  
 Lys Arg Lys Gln Ser His Pro Gly Ala Thr Pro Thr Val Gly Thr Pro  
 1185 1190 1195 1200  
 Ala Thr Lys Pro Pro Thr Thr Arg Pro Ala Asp Val Lys Met Pro  
 1205 1210 1215

<210> 35  
 <211> 1146  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 35  
 atgtcctac agttcgacgg ccggtctcca tatggctgcg tggagtgtca tccccagctg 60  
 atccagtgtg tcgacaagcc gtctcgttgc ccgtgccttt gcggcgccag catgacctgc 120  
 gactacatgg cgaccacccc agcgaactgg tccacgacta ccgagtcgcg gtcttcaccg 180  
 gcgatgacct ccattgcgga ccccatgaac caccgctcg ccacttcgc gctgcgggg 240  
 gagctgaacc acaccgagct cgagctgatg gtgcaatggt gcaccgacac ctaccgttcc 300  
 gtcgcgcacc agcccagcgt cgaatggatc tggcatgcg ccgtgcctcg ggaggccttg 360  
 caacggccct ttctctcca cggcatcctg gccgtctcgg ccctgcacct cttcttcgcg 420  
 accaccggcg acacgcaggc aactacttg cgtaccgccc acgcccacg acaacacgcc 480  
 gaggaaggcc tctcccaagc gtcgcgcgca ctggacgcct ccaactgcaa cgccgcgttc 540  
 gccgtctgca gcatgtcac cgtcttctcc tttgcctgc cgtggccgc gcgcgcacc 600  
 ccgacagccg cacacagtcc gctggacgag ctgtgtcaca tcatgaggca cagcaccag 660  
 tccatgagct ccctgtcgga gatcgtctac tgggtcggcc gcggcgacct ccacgcgtc 720  
 atcgagtgcg acgaaaccgc accccggatg ccggacacgt cgcggctcgc catcatgctg 780  
 ttggcgcgcc tgaacgatac cctggcgacg caatccccgc agcacgagaa gcgcgtattc 840  
 gaccgcgcc tcgacgcct gggccactca ctcgaccagc tcgcccgcgg cggcgagctt 900  
 ctctctcgg ccttcgggtg gattgtgcag atcccaccgc ggttcacgca gctcctccac 960

```

gagcggcatc cgtttgcgct ggtgatacctg gcgcactatg cggtcgtcct gcatctgctg 1020
cgggagcggtt ggtgggtggg tgactggggc gcacgggtga ttcaagcggg gggacggagt 1080
ttagaatggg agtggagaaa ggccctggga tgggtgttg atgcgacggg atgtattctg 1140
ccgcaa 1146

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&lt;210&gt; 36

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 36

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Met Leu Leu Gln Phe Asp Gly Arg Ser Pro Tyr Gly Cys Val Glu Cys
 1      5      10      15
His Pro Gln Leu Ile Gln Cys Val Asp Lys Pro Ser Arg Cys Pro Cys
      20      25      30
Leu Cys Gly Ala Ser Met Thr Cys Asp Tyr Met Ala Thr Thr Pro Ala
      35      40      45
Asn Trp Ser Thr Thr Thr Glu Ser Ala Ser Ser Pro Ala Met Thr Ser
      50      55      60
Ile Ala Asp Pro Met Asn His Pro Leu Ala His Phe Ala Pro Ala Gly
65      70      75      80
Glu Leu Asn His Thr Glu Leu Glu Leu Met Val Gln Trp Cys Thr Asp
      85      90      95
Thr Tyr Arg Ser Val Ala His Gln Pro Ser Val Glu Trp Ile Trp His
      100      105      110
Ala Ala Val Pro Arg Glu Ala Leu Gln Arg Pro Phe Leu Leu His Gly
      115      120      125
Ile Leu Ala Val Ser Ala Leu His Leu Phe Phe Arg Thr Thr Gly Asp
      130      135      140
Thr Gln Ala His Tyr Leu Arg Thr Ala His Ala His Arg Gln His Ala
145      150      155      160
Glu Glu Gly Leu Ser Gln Ala Leu Arg Ala Leu Asp Ala Ser Asn Cys
      165      170      175
Asn Ala Ala Phe Ala Val Cys Ser Met Leu Thr Val Phe Ser Phe Ala
      180      185      190
Leu Pro Leu Ala Ala Arg Arg Thr Pro Thr Ala Ala His Ser Pro Leu
      195      200      205
Asp Glu Leu Cys His Ile Met Arg His Thr His Gln Ser Met Ser Ser
210      215      220
Leu Cys Glu Ile Val Tyr Trp Val Gly Arg Gly Asp Leu His Ala Leu
225      230      235      240
Ile Glu Cys Asp Glu Thr Ala Pro Arg Met Pro Asp Thr Ser Arg Leu
      245      250      255
Ala Ile Met Ala Leu Ala Arg Leu Asn Asp Thr Leu Ala Thr Gln Ser
      260      265      270
Pro Gln His Glu Lys Arg Val Phe Asp Arg Ala Leu Asp Ala Leu Gly
      275      280      285
His Ser Leu Asp Gln Leu Ala Arg Gly Gly Glu Leu Leu Ser Ala
290      295      300
Phe Arg Trp Ile Val Gln Ile Pro Pro Arg Phe Ile Glu Leu Leu His
305      310      315      320
Glu Arg His Pro Phe Ala Leu Val Ile Leu Ala His Tyr Ala Val Val
      325      330      335
Leu His Leu Leu Arg Glu Arg Trp Trp Val Gly Asp Trp Gly Ala Arg

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          340          345          350
Val Ile Gln Ala Val Gly Arg Ser Leu Glu Trp Glu Trp Arg Lys Ala
          355          360          365
Leu Gly Trp Val Leu Asp Ala Thr Gly Cys Ile Leu Pro Gln
          370          375          380

```

<210> 37  
 <211> 540  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

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<400> 37
atgtccggct acaacaacca gtacaaccag ggctacggct acaaccaggg tggttatccc 60
ccgcagggtg gttactccca ggggtggctat ggtcagtcctc aggggtggtag cgccaacgat 120
tactacggcg gacagcagcc tcagcatcac cagcagcacg gatacaacca gtatgaccag 180
agccagcagg gttatgttca gcagcagcag tatggtcagc agcaatacgg tcagcaagg 240
catgatcaac aggtctcccg tgaagccag gagggcgagc gtggactgat gggcgctctg 300
gccggtggtg cagcgggttg ttctgccggt cacaaggcca accacggctt cctcggaacc 360
atcggcggtg ccatcatggg aagcatcgcg gaagatgcc acaagaagca caagaacaag 420
aacgagggtc cccccagta cggcagcaac tatggcggca gccagtatgg cgccctcct 480
ccctcccaag gaggtcttaa caacggcatg atgggaccagc tgggcagctt cttcaagaaa 540

```

<210> 38  
 <211> 180  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

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<400> 38
Met Ser Gly Tyr Asn Asn Gln Tyr Asn Gln Gly Tyr Gly Tyr Asn Gln
  1          5          10          15
Gly Gly Tyr Pro Pro Gln Gly Gly Tyr Ser Gln Gly Gly Tyr Gly Gln
          20          25          30
Ser Gln Gly Gly Ser Ala Asn Asp Tyr Tyr Gly Gly Gln Gln Pro Gln
          35          40          45
His His Gln Gln His Gly Tyr Asn Gln Tyr Asp Gln Ser Gln Gln Gly
          50          55          60
Tyr Gly Gln Gln Gln Gln Tyr Gly Gln Gln Gln Tyr Gly Gln Gln Gly
          65          70          75          80
His Asp Gln Gln Ala Pro Gly Glu Ala Gln Glu Gly Glu Arg Gly Leu
          85          90          95
Met Gly Ala Leu Ala Gly Gly Ala Ala Gly Gly Phe Ala Gly His Lys
          100          105          110
Ala Asn His Gly Phe Leu Gly Thr Ile Gly Gly Ala Ile Met Gly Ser
          115          120          125
Ile Ala Glu Asp Ala Ile Lys Lys His Lys Asn Lys Asn Glu Gly Pro
          130          135          140
Pro Glu Tyr Gly Ser Asn Tyr Gly Gly Ser Gln Tyr Gly Gly Pro Pro
          145          150          155          160
Pro Ser His Gly Gly Ser Asn Asn Gly Met Met Asp Gln Leu Gly Ser

```

165 170 175  
Phe Phe Lys Lys  
180

<210> 39  
<211> 1191  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fungal gene

<400> 39  
atgttcgcag aatcccaacc ccccgagcagc ggtggcgaca cccccaagct ccggggcggct 60  
tgtgagaact gccgtcagtc gaaagtgaag tgcaacctgg gaggaagaa cacctgcatac 120  
cgctgtcttc gccatggcct tccttgctga taccgggtcg ccaaccgatc cggcaagccg 180  
aaggggagca agaaccgagc tacgctgcga aagctgggcc agctccagga cgagaagccg 240  
gtgcagggct cgcacagcgc gcgggagccg aagaaggccg tggagccggt gtgtccgccg 300  
gagtatgagg tcgaccgcag attcgagtac cagacaagcg agccgagtcg gccgcggctg 360  
tctgagagtc cacatatgca cgactccac cgcacaatcg acgcctgcat gctagtgaat 420  
gagacgcca tcgactacac ggctacctat ggcggccgt tctccccgc catgccgatg 480  
tgacgcgg cgctgatgtc gccgacatcg cccaccttc tgcaaaagga gttcatcacg 540  
aaaggcctga ccagcttccc gctggccgtg cacgtccccg gcgccttacc gccgcgctgc 600  
gagtgcgacg aggcgctcgg cttccacttg aacggactgc gacatatggt ggtcgaccgc 660  
gcgcggctgc gcttcgacca gggcctgcag gcgatcaaga cggcgctcgc cgtatgtcag 720  
gggttcctgc ggtgcgcgcg ctgtccaaag ggcaacacga acttcctggt ctgcgtgtcg 780  
acgctggacc tcgtgctgca gctcttcgac ttctgggtga gttgcgagtt cgcagcccac 840  
ggccacggcc acgggcccgc ggcgtcgtcg ctggaggccg agcccatggc ttacggcgag 900  
tacgagacag cgcgcgagga ggcgcggcac atgcggcggg tgggtgctgcg cgggcgcctg 960  
ctgcagtgca aggaggtgct gggcctgctg cacgaggccg tggagctggc cgagggccag 1020  
ggcctgagca gtagcagcag cagtagcgag gcgctggacg ggagctggct gcagcagatc 1080  
atccgcgggt atgcgagcgc gacggagtcc ctctccagc cgctggggtg tatttgcgga 1140  
ggcagcgcgg tgcaactagc gcatagaccg agtaccgggt tagataggct g 1191

<210> 40  
<211> 397  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fungal gene

<400> 40  
Met Phe Ala Glu Ser Gln Pro Pro Ser Ser Gly Gly Asp Thr Pro Lys  
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20 25 30  
Leu Gly Gly Lys Asn Thr Cys Ile Arg Cys Leu Arg His Gly Leu Pro  
35 40 45  
Cys Arg Tyr Arg Val Ala Asn Arg Ser Gly Lys Pro Lys Gly Ser Lys  
50 55 60  
Asn Arg Ala Thr Leu Arg Lys Leu Gly Gln Leu Gln Asp Glu Lys Pro  
65 70 75 80  
Val Gln Gly Ser His Ser Ala Arg Glu Pro Lys Lys Ala Val Glu Pro  
85 90 95  
Val Cys Pro Pro Glu Tyr Glu Val Asp Arg Arg Phe Glu Tyr Gln Thr

				100						105				110		
Ser	Glu	Pro	Ser	Gln	Pro	Arg	Leu	Ser	Glu	Ser	Pro	His	Met	His	Asp	
		115					120					125				
Ser	His	Pro	Thr	Ile	Asp	Ala	Cys	Met	Leu	Val	Asn	Glu	Thr	Pro	Ile	
	130					135					140					
Asp	Tyr	Thr	Ala	Thr	Tyr	Gly	Gly	Pro	Phe	Ser	Pro	Ala	Met	Pro	Met	
145					150					155					160	
Cys	Thr	Pro	Ala	Ser	Met	Ser	Pro	Thr	Ser	Pro	Thr	Phe	Leu	Gln	Lys	
				165					170					175		
Glu	Phe	Ile	Thr	Lys	Gly	Leu	Thr	Ser	Phe	Pro	Leu	Ala	Val	His	Val	
			180					185					190			
Pro	Gly	Ala	Leu	Pro	Pro	Arg	Cys	Glu	Cys	Asp	Glu	Ala	Leu	Gly	Phe	
		195					200					205				
His	Leu	Asn	Gly	Leu	Arg	His	Met	Val	Val	Asp	Pro	Ala	Arg	Leu	Arg	
	210					215					220					
Phe	Asp	Gln	Gly	Leu	Gln	Ala	Ile	Lys	Thr	Ala	Leu	Ala	Val	Cys	Gln	
225					230					235					240	
Gly	Phe	Leu	Arg	Cys	Ala	Arg	Cys	Pro	Lys	Gly	Asn	Thr	Asn	Phe	Leu	
				245					250					255		
Val	Ser	Leu	Ser	Thr	Leu	Asp	Leu	Val	Leu	Gln	Leu	Phe	Asp	Phe	Trp	
			260					265					270			
Val	Ser	Cys	Glu	Phe	Ala	Ala	His	Gly	His	Gly	His	Gly	Pro	Pro	Ala	
		275					280					285				
Ser	Ser	Leu	Glu	Ala	Glu	Pro	Met	Ala	Tyr	Gly	Glu	Tyr	Glu	Thr	Ala	
						295					300					
Pro	Glu	Glu	Ala	Arg	His	Met	Arg	Arg	Val	Val	Leu	Arg	Gly	Arg	Leu	
305					310					315					320	
Leu	Gln	Cys	Lys	Glu	Val	Leu	Gly	Leu	Leu	His	Glu	Ala	Val	Glu	Leu	
				325					330					335		
Ala	Glu	Gly	Gln	Gly	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Glu	Ala	Leu	
			340					345					350			
Asp	Gly	Ser	Trp	Leu	Gln	Gln	Ile	Ile	Arg	Gly	Tyr	Ala	Ser	Ala	Thr	
						360						365				
Glu	Ser	Leu	Leu	Gln	Pro	Leu	Gly	Cys	Ile	Cys	Gly	Gly	Ser	Ala	Val	
						375					380					
Gln	Leu	Ala	His	Arg	Pro	Ser	Thr	Gly	Leu	Asp	Arg	Leu				
385					390					395						

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<210> 41
<211> 1155
<212> DNA
<213> Artificial Sequence
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<220>  
<223> fungal gene

<400>	41						
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aatcgcttgg	tctccgactg	ggagacggac	atggaatccc	actccgacaa	tgacatcagc	120	
cgcgaccgca	tgcgatcctc	catcgagctc	ccctctctgc	gcgaccactt	caagcaggac	180	
tccctcccac	ccttctcccc	gcgaccgcgc	gaactgctcc	cctccatcct	caaccactcg	240	
cccccaggtc	gctcctccac	tcttcccccc	atccagcaaa	agaagtggcc	gcgcccgcgc	300	
aaatcctcca	tctccggcgc	tgcgaagccc	aaacatgaac	gctccaagtc	caaggagtac	360	
ggtcgccgcc	ccagcttagg	cgatcgcaaa	gccttgtccg	ccgaacccca	gaccgcccgc	420	
tgggtctcagg	gcaagcgttg	ggaggtactg	atcgaagccg	cgacttcggc	gaccgagggc	480	
gcgacgaac	gccattctga	ggtcggtcgg	tcgcccacca	tccctccggt	gtccagcttc	540	

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acctccgccc ccattggggaa gaatcgctcg tcgcttcccc cgggattcca aggactacca 600
ccccccacct cgcatacgctc gttcccgcct catccctacg ccgcgtcgcc gttgaacaag 660
tccctgaccc caccgcccga cgacctcgcg cgcagccggg acaatgacct ggagcccttc 720
ccctcgatag agtcgtccct cgactccgcc tcgaccgcgt ccggaaagac cctccactat 780
aatcacgtcg gtccggccaa cgactccagt ccggtgctga acatgttccc gtcgtcggcc 840
gtgcagcgcc aacaccatcg cttttccaac cccacccccg cctccatgcg gagccgcgag 900
atccagatct attgcgccc ctgcaagcga ccgtgggcgc tcaacgaatg ctacgcctgc 960
accgagtgca tctgcggcgt ctgtcgcgaa tgtgtcggaa tggttcacgcg cagccccgcc 1020
acctccttcc gcaacgtcac ctccagcccc ggagtgccct tgccccacgg cccgaccagc 1080
tatcctagcg cccgaggttg tcccgcgtgt cgcaccgtcg gcggcaagtg gaaggctttt 1140
cagctggatt tcaag                                     1155

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<210> 42

<211> 385

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 42

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Met Asp Asp Thr His Pro Ala Ala Ala Thr Ala Ala Val Ala Leu Ala
 1          5          10          15
Gln Leu His His Asn Arg Leu Val Ser Asp Trp Glu Thr Asp Met Glu
          20          25          30
Ser His Ser Asp Asn Asp Ile Ser Arg Asp Arg Met Arg Ser Ser Ile
          35          40          45
Glu Leu Pro Ser Leu Arg Asp His Phe Lys Gln Asp Ser Leu Pro Pro
          50          55          60
Phe Ser Pro Arg Pro Arg Glu Leu Leu Pro Ser Ile Leu Asn His Ser
65          70          75          80
Pro Pro Gly Arg Ser Ser Thr Leu Pro Pro Ile Gln Gln Lys Lys Trp
          85          90          95
Pro Arg Pro Arg Lys Ser Ser Ile Ser Gly Ala Arg Lys Pro Lys His
          100          105          110
Glu Arg Ser Lys Ser Lys Glu Tyr Gly Arg Arg Pro Ser Leu Gly Asp
          115          120          125
Arg Lys Ala Leu Ser Ala Glu Pro Gln Thr Ala Ala Trp Ala Gln Gly
          130          135          140
Lys Arg Trp Glu Asp Leu Ile Glu Ala Ala Thr Ser Ala Thr Glu Ala
145          150          155          160
Asp Asp Glu Arg His Ser Glu Val Gly Arg Ser Pro Thr Ile Pro Pro
          165          170          175
Val Ser Ser Phe Thr Ser Ala Pro Met Gly Lys Asn Arg Ser Ser Leu
          180          185          190
Pro Pro Gly Phe Gln Gly Leu Pro Pro Pro Thr Ser His Arg Pro Phe
          195          200          205
Pro Pro His Pro Tyr Ala Ala Ser Pro Leu Asn Lys Ser Leu Thr Pro
          210          215          220
Pro Pro Tyr Asp Leu Ala Arg Ser Arg Asp Asn Asp Leu Glu Pro Phe
225          230          235          240
Pro Ser Ile Glu Ser Ser Leu Asp Ser Ala Ser Thr Ala Ser Gly Lys
          245          250          255
Thr Leu His Tyr Asn His Val Gly Pro Ala Asn Asp Ser Ser Pro Val
          260          265          270
Leu Asn Met Phe Pro Ser Ser Ala Val Gln Arg Gln His His Arg Phe
          275          280          285

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Ser Asn Pro Thr Pro Ala Ser Met Arg Ser Arg Glu Ile Gln Ile Tyr  
 290 295 300  
 Cys Ala His Cys Lys Arg Pro Trp Ala Leu Asn Glu Cys Tyr Ala Cys  
 305 310 315 320  
 Thr Glu Cys Ile Cys Gly Val Cys Arg Glu Cys Val Gly Met Phe Ile  
 325 330 335  
 Gly Ser Pro Pro Thr Ser Phe Arg Asn Val Thr Ser Ser Pro Gly Ser  
 340 345 350  
 Ala Leu Pro His Gly Pro Thr Ser Tyr Pro Ser Ala Arg Gly Cys Pro  
 355 360 365  
 Arg Cys Arg Thr Val Gly Gly Lys Trp Lys Ala Phe Gln Leu Asp Phe  
 370 375 380  
 Lys  
 385

<210> 43  
 <211> 1395  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 43  
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 gcccatctcc agcagcaaca gccccagcat catcccatg cccagtcggc caacacagct 120  
 cttccgcgcg cctcgcttgg cggccatccc ggcttcgcgc ccagcaccaa caccaacatg 180  
 aacccttcca cgttatccgg caccgggcatc gcgaatggca tgtcggtcgc tgcgtttggc 240  
 ggcgacggtg gaggcacggg ccttgccagt catgccgcgc agatgggggt cgcgagaggg 300  
 gcacagatgc agcaacagca gttacatcag gccacgacg gccgactagc cctcgagacc 360  
 aaagccggtg gcgtcaaaac gcggatacga gacgtatgga agcataatct tgctcaggaa 420  
 atggcgatcc tcagacaact ggtggagaag tatccctaca tcagcatgga taccgagttt 480  
 cccggcatcg tcgctcgctc cattggcgcc ttacgaata aagcggacta ccaactacaa 540  
 acccttcgat gtaacgtcga cctggtgaag atgatccagc tgggaatcac ccttttttct 600  
 tccgaaggag aagttcctcc ccccaatgcc accgatgcga atggacagcc gctcggaaac 660  
 ggtctggtac ctgcgccctg cacctggcag ttcaacttcc ggttttcggt ggaggatgac 720  
 atgtacgccc aagagtcaac ggcgatggtg gcgaaggccg gtatcgattt cgccatgcac 780  
 gacaagaatg gaatcgatcc ctttgagtgc ggccgctct tgatcagctc aggcctcgct 840  
 ctctcgatg acgtccactg ggtttcgttc cactccggtc acgatttcggt ctatttgatg 900  
 aagattatgc tctgcaaacc tctcccgag aacgaagagg aatttcacag gcttctcaac 960  
 atcttcttcc cgtcattata cgatattaaa tacctgatga agcatgcggg tcgcaatcaa 1020  
 gccaagtccg gattgcaaga tattgcgac gagctggcg tcaagcgtgt cgggattgct 1080  
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 gtcttcaacg gaaacatcga cgaagcgaaa tactccggtc agatctgggg gctgaacggc 1200  
 caaatgccag cgctgctgta ttctatgcag ccccatcaga cccccaatct caacggggct 1260  
 accatctatt cggccactgg caccgccagt acgccaatg ctgttcattc tgtcacgggc 1320  
 agccacacac cccagcatgc actgacaccc ggtgccaccg gcgggggtgtt gggacagttc 1380  
 catgaggcaa agtca 1395

<210> 44  
 <211> 465  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

&lt;400&gt; 44

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Met Pro Pro Pro Val Gly Arg Tyr Gly Met Gly Ala Ala Pro Phe Ala
 1          5          10          15
His Leu Gln Gln Ala His Leu Gln Gln Gln Gln Pro Gln His His Pro
          20          25          30
His Ala Gln Ser Ala Asn Thr Ala Leu Pro Pro Pro Ser Leu Gly Gly
          35          40          45
His Pro Gly Phe Ala Ala Ser Thr Asn Thr Asn Met Asn Pro Phe Thr
          50          55          60
Leu Ser Gly Thr Gly Ile Ala Asn Gly Met Ser Val Ala Ala Phe Gly
65          70          75          80
Gly Asp Gly Gly Gly Thr Gly Leu Ala Ser His Ala Ala Gln Met Gly
          85          90          95
Phe Ala Arg Gly Ala Gln Met Gln Gln Gln Gln Leu His Gln Ala His
          100          105          110
Asp Gly Arg Leu Ala Leu Glu Thr Lys Ala Gly Gly Val Lys Thr Arg
          115          120          125
Ile Arg Asp Val Trp Lys His Asn Leu Ala Gln Glu Met Ala Ile Leu
          130          135          140
Arg Gln Leu Val Glu Lys Tyr Pro Tyr Ile Ser Met Asp Thr Glu Phe
145          150          155          160
Pro Gly Ile Val Ala Arg Pro Ile Gly Ala Phe Thr Asn Lys Ala Asp
          165          170          175
Tyr His Tyr Gln Thr Leu Arg Cys Asn Val Asp Leu Leu Lys Met Ile
          180          185          190
Gln Leu Gly Ile Thr Leu Phe Ser Ser Glu Gly Glu Val Pro Pro Pro
          195          200          205
Asn Ala Thr Asp Ala Asn Gly Gln Pro Leu Gly Asn Gly Leu Val Pro
          210          215          220
Ala Pro Cys Thr Trp Gln Phe Asn Phe Arg Phe Ser Leu Glu Asp Asp
225          230          235          240
Met Tyr Ala Gln Glu Ser Thr Ala Met Leu Ala Lys Ala Gly Ile Asp
          245          250          255
Phe Ala Met His Asp Lys Asn Gly Ile Asp Pro Phe Glu Phe Gly Ala
          260          265          270
Leu Leu Ile Ser Ser Gly Leu Val Leu Leu Asp Asp Val His Trp Val
          275          280          285
Ser Phe His Ser Gly Tyr Asp Phe Gly Tyr Leu Met Lys Ile Met Leu
          290          295          300
Cys Lys Pro Leu Pro Glu Asn Glu Glu Glu Phe His Arg Leu Leu Asn
305          310          315          320
Ile Phe Phe Pro Ser Leu Tyr Asp Ile Lys Tyr Leu Met Lys His Ala
          325          330          335
Gly Arg Asn Gln Ala Lys Ser Gly Leu Gln Asp Ile Ala Asp Glu Leu
          340          345          350
Gly Val Lys Arg Val Gly Ile Ala His Gln Ala Gly Ser Asp Ser Leu
          355          360          365
Val Thr Gly Glu Ile Tyr Trp Lys Met Arg Gln Leu Val Phe Asn Gly
          370          375          380
Asn Ile Asp Glu Ala Lys Tyr Ser Gly Gln Ile Trp Gly Leu Asn Gly
385          390          395          400
Gln Met Pro Ala Leu Leu Tyr Ser Met Gln Pro His Gln Thr Pro Asn
          405          410          415
Leu Asn Gly Ala Thr Ile Tyr Ser Ala Thr Gly Thr Pro Ser Thr Pro
          420          425          430
Asn Ala Val His Ser Val Thr Gly Ser His Thr Pro Gln His Ala Leu

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435                      440                      445  
 Thr Pro Gly Ala Thr Gly Gly Val Leu Gly Gln Phe Gln Met Ala Lys  
 450                      455                      460  
 Ser  
 465

<210> 45  
 <211> 1518  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 45  
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 tatctggcca tgcaattcga tccgaataaa cccggcgcac gagaccggtt tggatcgacg 180  
 ggggctttcg gtcccaatgg cgggtatccc cactgactcg cccctctggt caaagttgtg 240  
 attcaccatt tcacctgccg ctctttgacc atcggtagct ggcgcgcgat tggacagaac 300  
 gcgatggact tggatggttt ctactcccc gagaaggctt gcatgacctt ctatatcaac 360  
 aacgactcgg ccggctacaa aatcgagtag ccttttgctt acattaaaaa catcacgctg 420  
 gaatcgggcg atcagacagc gcagcccaac ggagcgcccc cgcgcccggg cgggtctcatt 480  
 gttgaattga accgcccggc gctctttctac atggattcct ccaactccgg tggcttctac 540  
 cagtgcggcg acttcaccga ggaccagcag gccagccagc tgttgggtgca ccactctggc 600  
 ggccacccca aagtcctgag cgtccagctg gccaaagctg tctcgttga gtcgttccag 660  
 aaccgtcttg cctacaacaa cttcgccatg agtgcgccc tgtcccggc ttttatccag 720  
 cggcccgctt cccagccgaa tcagtttgcc cggcggttg tgggcatgta tgcggagaac 780  
 cccgcgacgc tgagcctgca gcaggcggcg cgcggacaca agcgccaacg cagccgttcg 840  
 gtgcccgtag ccgtcgactt ctcggccatg cagaccccca tgtcgtacca gatgcagaac 900  
 ccgtcgagat tcaaccagcc agattcgagt atctttgccc ccgttcgcga gtcgacccat 960  
 ccaactggcg tgaacctgcg catcgatacg tcggccccct acggcttcga cccgcgcggc 1020  
 catcccattg cggcgccac caggaactca ccctcggaat ttgccagtc ctcgctattc 1080  
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 atgcccattg tgtcccggc ggtggactcg tctacgctcg ccaccaggc cgcgtcgccg 1200  
 tactccacgg tcagccacgc ggaccccatg attgcccacc agtcccctcc catgaccaac 1260  
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 gagaacatgt ccatgagcgg catgttcccc aagcacaaca tgaatttctc ggtaccacc 1380  
 acgatggacg tcggaggcaa cacctttgat ctcccatc agaccctgtc caaccaccg 1440  
 tccccggggg ttcagggtga ctaccaaagc atgactccgc tggagaatgt cgatcccaac 1500  
 acgtggctc ctggggcg 1518

<210> 46  
 <211> 506  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 46  
 Met Thr Glu Arg Ser Val Gln Ile Trp Phe Gln Asn Arg Arg Ala Lys  
 1                      5                      10                      15  
 Ile Lys Met Leu Ala Lys Lys Ser Ile Glu Thr Gly Glu Gly Cys Asp  
 20                      25                      30  
 Ser Ile Pro Glu Ser Met Arg Gln Tyr Leu Ala Met Gln Phe Asp Pro

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Val Asp Pro Asn Thr Leu Ala Pro Gly Ala  
500 505

<210> 47  
<211> 1731  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fungal gene

<400> 47  
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cttcagaaga gtgtgctgca gaacaatacc tctggcctct ctcaacaaca aatcgcccaa 120  
ctccagaaga accaacattt gcagatgatg cagatgcaaa gagatcagtc cgagatggac 180  
atgaatggtc accgtcccca gtcccctgcg tctgccgaga acgccccttc cccatccaag 240  
cggccccgtc tggaaggcgg accgatgaac ggacaacagt tagcgcctaa cggacgtggt 300  
caagcacagg gaatgcccgg tcaaccgaat ccgcaggccc tttttatgca gaatgggggt 360  
ctcaaccac gaggaatgaa ccgggccaa cttcaggctt tccagcaggg tccgggcgcg 420  
cagcagaaat caatccaggg catgccgaat ggcattatga atcccgggtg gatgccaaac 480  
cagacggatc tgatgcccac gccagaaggc cagggtatgt acccgatgaa cggtgactac 540  
tatggcgcgga atgggtcaaat ggcccagggt cgggctggga tgcagacgcc tggcaatcag 600  
ggaaaccatg ctcttcagga ttatcagatg cagcttatgt tgctggaaca gcagaataag 660  
cgacgtttga tgatggctcg ccaagagcag gatagcatgg ctcgtcctga cggccagccc 720  
ccaatgcctg ggcagcagca gttgccgcca ggcacctctc cccaaggcag caggggcgggc 780  
gcctctccga accccaacga tcagatgaag aggggtacac cgaagatgcc gcagaccggt 840  
cttcagggt ctccgaatcc tggcgatgtc gctcaagggt gtggatcccc ggcttccatg 900  
aatttcaaca gcgcccagat gccaccgcac atgacgaacc cattcttcgc cgctccgaac 960  
ggtatgcgac ccccgagctc gaaccgcgca tttaccaccg gtccgccgat gggccagcaa 1020  
attcctgcag gtgcccagat gccgaatcgc gcttggcagc cgcagcaggg cgctcagggc 1080  
caacctatgc cccacagca gtcccctgcg gcgcagccgg ccacgggaac tccccaggaa 1140  
cgcaacaaa tgccgcccgc ccaggctcct ccgctgctg ggcctaattc cggacgcacg 1200  
cagccgccgt ctctcagac cggagccgct gccctccca cgcgccagca atccaacaag 1260  
gccgcaccca aggggaagaa agacacgaag gacactaatc ggaagcggcc gaagaaggca 1320  
gctggccctg cagcggtcgc agctgcctcg aatactgccg cgacccctc gtccgaggct 1380  
gagcatgcga cgacgccgtc gacgcgatc acgctcagc atccgaactc gttcaacaag 1440  
ccggggccca ataccagcag gagtgcgccc cagcaaccca catcggcgcc tgcgcaccg 1500  
acgtggtgac agccgcccgc acccgaccag aaccagccgt tcaatgacct tagcatgcca 1560  
gacgcgtctg ctttcaacct ggacttcagc gccctggaga atccggacat tttggagaac 1620  
ttcgacttgc atacctttct caacactgac gcggatacgg cggggtttgg gtttgatccc 1680  
aacatgccat atcctgggga cggcgttgag actggtgccg gagaaggtct g 1731

<210> 48  
<211> 577  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fungal gene

<400> 48  
Met Met Pro Ala Gln Met Arg Gln Leu Asn Met Arg Gly Asn Ala Met  
1 5 10 15  
Val Pro Pro Asn Leu Gln Lys Ser Val Leu Gln Asn Asn Thr Ser Gly  
20 25 30  
Leu Ser Gln Gln Gln Ile Ala Gln Leu Gln Lys Asn Gln His Leu Gln

	35						40						45					
Met	Met	Gln	Met	Gln	Arg	Asp	Gln	Ser	Glu	Met	Asp	Met	Asn	Gly	His			
	50					55					60							
Arg	Pro	Gln	Ser	Pro	Ala	Ser	Ala	Glu	Asn	Ala	Pro	Ser	Pro	Ser	Lys			
65					70					75					80			
Arg	Pro	Arg	Leu	Glu	Gly	Gly	Pro	Met	Asn	Gly	Gln	Gln	Leu	Ala	Pro			
				85					90					95				
Asn	Gly	Arg	Gly	Gln	Ala	Gln	Gly	Met	Pro	Gly	Gln	Pro	Asn	Pro	Gln			
			100					105					110					
Ala	Leu	Phe	Met	Gln	Asn	Gly	Gly	Leu	Asn	Pro	Arg	Gly	Met	Asn	Pro			
		115					120					125						
Ala	Gln	Leu	Gln	Ala	Phe	Gln	Gln	Gly	Pro	Gly	Ala	Gln	Gln	Lys	Ser			
	130					135					140							
Ile	Gln	Gly	Met	Pro	Asn	Gly	Ile	Met	Asn	Pro	Gly	Val	Met	Pro	Asn			
145					150					155					160			
Gln	Thr	Asp	Leu	Met	Pro	Met	Pro	Glu	Gly	Gln	Gly	Met	Tyr	Pro	Met			
				165					170					175				
Asn	Gly	Asp	Tyr	Tyr	Gly	Ala	Asn	Gly	Gln	Met	Ala	Gln	Val	Arg	Ala			
			180					185					190					
Gly	Met	Gln	Thr	Pro	Gly	Asn	Gln	Gly	Asn	His	Ala	Leu	Gln	Asp	Tyr			
		195					200					205						
Gln	Met	Gln	Leu	Met	Leu	Leu	Glu	Gln	Gln	Asn	Lys	Arg	Arg	Leu	Met			
	210					215					220							
Met	Ala	Arg	Gln	Glu	Gln	Asp	Ser	Met	Ala	Arg	Pro	Asp	Gly	Gln	Pro			
225					230					235					240			
Pro	Met	Pro	Gly	Gln	Gln	Gln	Leu	Pro	Pro	Gly	Thr	Ser	Pro	Gln	Gly			
				245					250					255				
Ser	Arg	Ala	Gly	Ala	Ser	Pro	Asn	Pro	Asn	Asp	Gln	Met	Lys	Arg	Gly			
			260					265					270					
Thr	Pro	Lys	Met	Pro	Gln	Thr	Gly	Leu	Pro	Gly	Ser	Pro	Asn	Pro	Gly			
		275					280					285						
Asp	Val	Ala	Gln	Gly	Arg	Gly	Ser	Pro	Ala	Ser	Met	Asn	Phe	Asn	Ser			
	290					295					300							
Ala	Gln	Met	Pro	Pro	Asp	Met	Thr	Asn	Pro	Phe	Phe	Ala	Ala	Pro	Asn			
305					310					315					320			
Gly	Met	Arg	Pro	Pro	Ser	Ser	Asn	Pro	Ala	Phe	Thr	Thr	Gly	Pro	Pro			
				325					330					335				
Met	Gly	Gln	Gln	Ile	Pro	Ala	Gly	Ala	Gln	Met	Pro	Asn	Arg	Ala	Trp			
			340					345					350					
Gln	Pro	Gln	Gln	Gly	Ala	Gln	Gly	Gln	Pro	Met	Pro	Pro	Gln	Gln	Ser			
		355					360					365						
Pro	Ala	Ala	Gln	Pro	Ala	Thr	Gly	Thr	Pro	Gln	Glu	Arg	Asn	Gln	Met			
	370					375					380							
Pro	Pro	Pro	Gln	Ala	Pro	Pro	Ala	Ala	Gly	Pro	Asn	Ser	Gly	Arg	Thr			
385					390					395					400			

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Pro Ala Ala Pro Thr Leu Val Gln Pro Pro Pro Pro Asp Gln Asn Gln
      500      505      510
Pro Phe Asn Asp Leu Ser Met Pro Asp Ala Ser Ala Phe Asn Leu Asp
      515      520      525
Phe Ser Ala Leu Glu Asn Pro Asp Ile Leu Glu Asn Phe Asp Phe Asp
      530      535      540
Thr Phe Leu Asn Thr Asp Ala Asp Thr Ala Gly Phe Gly Phe Asp Pro
545      550      555      560
Asn Met Pro Tyr Pro Gly Asp Gly Val Glu Thr Gly Ala Gly Glu Gly
      565      570      575
Leu

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<210> 49
<211> 1152
<212> DNA
<213> Artificial Sequence

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<220>
<223> fungal gene

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<400> 49
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gggtatttcg aaagcctttt caatctccac aatctcatcc atgcgcagtc cgagttggtc 180
cgcatacaagg gtctcaattc gcttcttgac caagtaggtc accaggagca tttgtacgag 240
atctttgtag atgcaaccga gagtgtcttt gagcaagtgt gtgaggcgat tcaggccggg 300
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gccttcctgc cgtccccct cgatcagtac tgcacgacgc ggatcgagac cgtcaaaacg 480
gaaattgatg aagtgggcct ccaagctctg gtggacggcg tcatcgagcc gtccggcggt 540
gctgtcgaga tcctgtacct ggaccggagt cagggcgaag cagtcactcc ccatctcttg 600
accccgagtc ggcctagcgc ttcgacaatc cgtttgctgt atcgccctgg ccactacgat 660
attgctgacc aagcgggaacc taccgtgaca atggaaccca tcgtcaatta tcagtacggc 720
atgaccacca actactcgcc ctgggaccaa ggcgcctctt cgtttgatgt gaactcgagt 780
ctcatgtcca ttcccaacct gatgatggac cctccttttg cgctctcccc ttcccccatg 840
actccgctc cgagcccgta ccgcgtctcg cccctcagg aagtgttcca acctccgatg 900
cacacgcctc cgccaccggt ccccgtcgca tcgccgccac caccgccgat gtcagccccg 960
cccccgatga cttcggtacc taaccggtcc tcagacgggc cgcagattcg actgaatccg 1020
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gattcccgca aa 1152

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<210> 50
<211> 384
<212> PRT
<213> Artificial Sequence

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<220>
<223> fungal gene

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<400> 50
Met Glu Tyr Ser Gly Ala Asp Pro Thr Phe Val Ala Lys Thr Ser Ala
 1           5           10           15
Leu Ala Val Thr His Pro Phe Cys Arg Ile Met Lys Arg Asp Gly Asn
      20      25      30

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Cys Gly Trp Arg Ala Ala Ala Phe Gly Tyr Phe Glu Ser Leu Phe Asn  
 35 40 45  
 Leu His Asn Leu Ile His Ala Gln Ser Glu Leu Val Arg Ile Lys Gly  
 50 55 60  
 Leu Asn Ser Leu Leu Asp Gln Val Gly His Gln Glu His Leu Tyr Glu  
 65 70 75 80  
 Ile Phe Val Asp Ala Thr Glu Ser Val Phe Glu Gln Val Cys Glu Ala  
 85 90 95  
 Ile Gln Ala Gly Val Arg Asp Asp Ser Phe Leu Lys Asp Leu Phe Asn  
 100 105 110  
 Glu Glu Phe Asn Ser Ser Ala Val Ile Thr His Phe Arg Leu Leu Thr  
 115 120 125  
 Ser Ala Trp Met Lys Leu Asn Pro His Arg Tyr Gln Ala Phe Leu Pro  
 130 135 140  
 Leu Pro Leu Asp Gln Tyr Cys Thr Thr Arg Ile Glu Thr Val Lys Thr  
 145 150 155 160  
 Glu Ile Asp Glu Val Gly Leu Gln Ala Leu Val Asp Gly Val Ile Glu  
 165 170 175  
 Pro Ser Gly Val Ala Val Glu Ile Leu Tyr Leu Asp Arg Ser Gln Gly  
 180 185 190  
 Glu Ala Val Thr Pro His Leu Leu Thr Pro Ser Arg Pro Ser Ala Ser  
 195 200 205  
 Thr Ile Arg Leu Leu Tyr Arg Pro Gly His Tyr Asp Ile Ala Tyr Gln  
 210 215 220  
 Ala Glu Pro Thr Val Thr Met Glu Pro Ile Val Asn Tyr Gln Tyr Gly  
 225 230 235 240  
 Met Thr Thr Asn Tyr Ser Pro Trp Asp Gln Gly Ala Leu Ser Phe Asp  
 245 250 255  
 Val Asn Ser Ser Leu Met Ser Ile Pro Asn Leu Met Met Asp Pro Ser  
 260 265 270  
 Phe Ala Leu Ser Pro Ser Pro Met Thr Pro Ala Pro Ser Pro Tyr Arg  
 275 280 285  
 Val Ser Pro Pro Gln Glu Val Phe Gln Pro Pro Met His Thr Pro Pro  
 290 295 300  
 Pro Pro Val Pro Val Ala Ser Pro Pro Pro Pro Arg Met Ser Ala Pro  
 305 310 315 320  
 Pro Pro Met Thr Ser Leu Pro Asn Arg Ser Ser Asp Gly Pro Gln Ile  
 325 330 335  
 Arg Leu Asn Pro Leu Val Met Lys Gln Asn Leu Ser His Ser Leu Pro  
 340 345 350  
 Val Thr Thr Pro Phe Lys Asn Ser Pro Tyr Asn Gln Ala His Phe Gln  
 355 360 365  
 Asn Gln Asp Phe Glu Pro Ile His Trp Glu Pro Ser Asp Ser Arg Lys  
 370 375 380

<210> 51

<211> 2388

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 51

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 gtaggagctc atacggaccg ggctcttcag aatacctctg ggaacgtgca gtcctattca 120

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gacaatctcg cccccaacga cacgacgggg cgagatagtg gacatctgca gccgtatgct 180
cccaagtatc ctccctccgt cccaatccct gccatccctg tcccttcggc tgcgggccagc 240
ctgcaccatc aacacatcct agccaaccga tggcagcaga agaagctccg tcgacttcag 300
tccctggggc ccaaccagct gggttggtccc cgtcggggaa gaagctatct caagtcccag 360
aagtacctgg agtatcgagc gcggcctcga cgggacacgg gcaaggatgg ggagcctgtc 420
tggtcggatg agctggagga tgccttccaa caagcactcg aggcaaacc tcccatgggc 480
cggagaaagt ggtccgaacg gggcaaatcc tatggtcgaa acgagctgat tgcagagttt 540
atctacaagg ctacgggcaa gaggagaact aggaacaag tgtccagtca cctgcagggtg 600
ctcgactcgt tcctcaaggg ggaccctgac tgggaaagac tggtagcgga acagccgaca 660
gaccgctctg cagcccagcc tcaagcagct ggcccaagggt ggcggacctc catggaacac 720
cccctgtcaa gtcactacaa tcctctccac gctccttacc atgatcctct gcgacctgtg 780
cagccttacg tgggggagct gcctccccct tcctttgccc ccaaccccaa cgtccatgat 840
gccaacatca acaccgtcca gggcctcaat tttgacatgt gggtcagtgc accgaaccag 900
ccggaccgca ttgagaatgc tttccatgta tacaccgct tgcaggcgca ccaacgccat 960
cccgtggccc cttcaatgcc gttggagaac atcgtcgggt ggcggacctc cttcccttat 1020
ctgaattccc tgatggcgga cccaactgct tccctgaact gcgagatcat cctcctcgaa 1080
gccaacctcg agttgatgga cgactttcct ccgtccgggt cgcggctggg gatccagctg 1140
gagctggact ttgcccattc cgctgtgggc gatgcaccag tcagtcatat ggacaactgg 1200
tcttgacaga cctacatgta tgaggagagc cagaagatcc tggaggtcaa ccacagcctt 1260
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gacgagcaca cgcggcactt cttccggacc atgtctcgcg tgcaggagat ccgtgctacg 1440
tctcccaact cccgtcgact ctccagccac tacggcggt cctcgtgcga cgagagtaag 1500
cgggtcgcga tcttgctctg gaagttccgc cagacgcggc ctggggaggt tggcaccacg 1560
acctggcgga gactctttcc gccgcgggac cgcacgtcca ccaatagccc tcgtccggcg 1620
acgggcatcg acctcccccc gctgtcactg gactcgatcc tgctcaacaa gcccgcaccc 1680
aacgtctacc aagcgctcc gccgcagcca cacgaattga tgcaccacca cggcgcgctc 1740
cagcctcctt ggcagatgta cccaccccg catgatcaca tgtaccacac ggggagcttt 1800
gatcttctca actcgatctc gaaaccggag gacggcctgg gtgacaagac ggcggtctcg 1860
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aatggcagca acggcggtcc gatcatgtct aacgtgccgg acatgtcgtt gtcgcaccac 1980
aacctggggg gatacacaat gggccacgag agccaccact acgtgccgcc accgcagcaa 2040
cacggggtgc atgtccccga caacaacagc gttctgaata acatctttgc ctccggaccg 2100
cagtcgttcg aggagctggg ccataacagc cacgcgcggt ggtcgggacc gtccacgacc 2160
ctcccgtcgg acgtgggatc caacagctac ggcatcttt cctatcagtc cgaccagcac 2220
ccgcccgcga cgcgcgagcc ccatcagttc aacggcttcg agggcctgat ggggacggat 2280
ctgatggaca agctcgtggg caacatgccg ggcgaccctg gcttgaatgg ggcaggcccc 2340
gatcacgcca catccgcgta ccctgagaac agcacggttg aggcggtt 2388

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<210> 52

<211> 796

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 52

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Met Ala Thr Thr Asp Trp Gln Pro Asp Phe Val Pro Pro Asn Pro Pro
 1             5             10             15
Ala Leu Glu Ser Val Gly Ala His Thr Asp Arg Ala Leu Gln Asn Thr
                20             25             30
Ser Gly Asn Val Gln Ser Tyr Ser Asp Asn Leu Ala Pro Asn Asp Thr
                35             40             45
Thr Gly Arg Asp Ser Gly His Leu Gln Pro Tyr Ala Pro Lys Tyr Pro
                50             55             60
Pro Pro Leu Pro Ile Pro Ala His Pro Val Pro Ser Ala Ala Ala Ser

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65					70					75				80
Leu	His	His	Gln	His	Ile	Leu	Ala	Asn	Arg	Trp	Gln	Gln	Lys	Lys
				85										95
Arg	Arg	Leu	Gln	Ser	Leu	Gly	Pro	Asn	Gln	Leu	Val	Gly	Pro	Arg
			100					105					110	
Gly	Arg	Ser	Tyr	Leu	Lys	Ser	Gln	Lys	Tyr	Leu	Glu	Tyr	Arg	Ala
			115				120					125		
Pro	Arg	Arg	Asp	Thr	Gly	Lys	Asp	Gly	Glu	Pro	Val	Trp	Ser	Asp
			130			135					140			
Leu	Glu	Asp	Ala	Phe	Gln	Gln	Ala	Leu	Glu	Ala	Asn	Pro	Pro	Met
145					150					155				160
Arg	Arg	Lys	Trp	Ser	Glu	Arg	Gly	Lys	Ser	Tyr	Gly	Arg	Asn	Glu
				165					170					175
Ile	Ala	Glu	Phe	Ile	Tyr	Lys	Ala	Thr	Gly	Lys	Arg	Arg	Thr	Arg
			180				185						190	
Gln	Val	Ser	Ser	His	Leu	Gln	Val	Leu	Asp	Ser	Phe	Leu	Lys	Gly
			195				200					205		
Pro	Asp	Trp	Glu	Arg	Leu	Val	Arg	Glu	Gln	Pro	Thr	Asp	Arg	Ser
			210			215					220			
Ala	Gln	Pro	Gln	Ala	Ala	Gly	Pro	Arg	Trp	Arg	Thr	Ser	Met	Glu
225					230					235				240
Pro	Leu	Ser	Ser	His	Tyr	Asn	His	Leu	His	Ala	Pro	Tyr	His	Asp
				245					250					255
Leu	Arg	Pro	Val	Gln	Pro	Tyr	Val	Gly	Glu	Leu	Pro	Pro	Pro	Ser
			260					265					270	
Ala	Pro	Asn	Pro	Asn	Val	His	Asp	Ala	Asn	Ile	Asn	Thr	Val	Gln
		275					280					285		
Leu	Asn	Phe	Asp	Met	Trp	Val	Ser	Ala	Pro	Asn	Gln	Pro	Asp	Arg
					295					300				
Glu	Asn	Ala	Phe	His	Val	Tyr	Thr	Arg	Leu	Gln	Gly	Asp	Gln	Arg
305					310					315				320
Pro	Val	Ala	Pro	Ser	Met	Pro	Leu	Glu	Asn	Ile	Val	Gly	Trp	Arg
				325					330					335
Tyr	Phe	Pro	Tyr	Leu	Asn	Ser	Leu	Met	Ala	Asp	Pro	Thr	Ala	Ser
			340					345					350	
Asn	Cys	Glu	Ile	Ile	Leu	Leu	Glu	Ala	Asn	Leu	Glu	Leu	Met	Asp
			355				360					365		
Phe	Pro	Pro	Ser	Gly	Ser	Arg	Leu	Gly	Ile	Gln	Leu	Glu	Leu	Asp
			370			375					380			
Ala	His	Ser	Ala	Val	Gly	Asp	Ala	Pro	Val	Ser	Gln	Met	Asp	Asn
385					390					395				400
Ser	Cys	Ser	Thr	Tyr	Met	Tyr	Glu	Glu	Ser	Gln	Lys	Ile	Leu	Glu
				405					410					415
Asn	His	Ser	Leu	Ser	Lys	Pro	Ala	Ser	Thr	Lys	Val	Lys	Pro	Pro
			420					425					430	
Glu	Ser	Leu	Trp	Trp	Ala	Lys	Leu	Phe	Thr	Gln	Leu	Thr	Gln	Glu
			435			440						445		
Gln	Met	Ala	Glu	Lys	Ala	Gly	Gln	His	His	Ala	Ala	Asp	Glu	His
			450			455					460			
Arg	His	Phe	Phe	Arg	Thr	Met	Ser	Ala	Val	Gln	Glu	Ile	Arg	Ala
465					470					475				480
Ser	Pro	Asn	Ser	Arg	Arg	Leu	Ser	Ser	His	Tyr	Gly	Gly	Ser	Ser
				485					490					495
Asp	Glu	Ser	Lys	Arg	Val	Ala	Ile	Leu	Leu	Trp	Lys	Phe	Arg	Gln
			500					505					510	
Arg	Pro	Gly	Glu	Val	Gly	Thr	Thr	Thr	Trp	Arg	Arg	Leu	Phe	Pro
			515				520					525		



```

Pro Asp Arg Thr Ser Thr Asn Ser Pro Arg Pro Ala Thr Gly Ile Asp
 530          535          540
Leu Pro Pro Leu Ser Leu Asp Ser Ile Leu Leu Asn Lys Pro Ala Pro
545          550          555          560
Asn Val Tyr Gln Ala Pro Pro Pro Gln Pro His Glu Leu Met His His
          565          570          575
His Gly Ala Ser Gln Pro Pro Trp Gln Met Tyr Pro Pro Pro His Asp
          580          585          590
His Met Tyr Pro Thr Gly Ser Phe Asp Leu Leu Asn Ser Ile Ser Lys
          595          600          605
Pro Glu Asp Gly Leu Gly Asp Lys Thr Ala Val Ser Ser Val Ile Asp
610          615          620
Pro Phe Pro Asn Met Gln Gln His Glu Thr Ser Gln Pro Pro Asn Leu
625          630          635          640
Asn Gly Ser Asn Gly Gly Pro Ile Met Leu Asn Val Pro Asp Met Ser
          645          650          655
Leu Ser His His Asn Leu Gly Gly Tyr Thr Met Gly His Glu Ser His
          660          665          670
His Tyr Val Pro Pro Pro Gln Gln His Gly Val His Val Pro Asp Asn
          675          680          685
Asn Ser Val Leu Asn Asn Ile Phe Ala Ser Gly Pro Gln Ser Phe Glu
690          695          700
Glu Leu Gly His Asn Ser His Ala Ala Trp Ser Gly Pro Ser Thr Thr
705          710          715          720
Leu Pro Ser Asp Val Gly Ser Asn Ser Tyr Gly His Leu Ser Tyr Gln
          725          730          735
Ser Asp Gln His Pro Pro Ala Thr Arg Glu Pro His Gln Ser Asn Gly
          740          745          750
Phe Glu Gly Leu Met Gly Thr Asp Leu Met Asp Lys Leu Val Gly Asn
          755          760          765
Met Pro Gly Asp Pro Gly Leu Asn Gly Ala Gly Pro Asp His Ala Thr
770          775          780
Ser Ala Tyr Pro Glu Asn Ser Thr Val Glu Ala Val
785          790          795

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<210> 53

<211> 1431

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 53

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atgccacctc ccgtcggcag atatgcgccg tctggcttaa acgctccata caacatacaa 60
caagctcacc ttcaatctca acatcccgca cagcgacagt ccggaacac actccctccc 120
ccttcgcttg gtcatecttg tttcgcgggc aatccgaata ccaacatcaa cccttttaca 180
ctatccggcg gaattgcaaa tggtagggcg gtagccggct tcccgggagc tggtagcagg 240
gatggcgggc gcaccgggtc ggctagtcac gcggcacaga tgggattcgc gcgcgggtgc 300
caaatgcaac aacagcaact acaccagggc cacgacggtc ggtagcgcgt cgaagcaaag 360
ggcgggtgcag tgaagtcaag aattagagat gtctggaagc acaacctggc ccatgagatg 420
gcgggtgctg ggcagttggc cgacaagtac ccttacatca gcatggacac cgagttccct 480
ggtagtggtg ctgggccgat aggggtcttt tcgaacaaag ccgattacca ttatcagacc 540
ctccgatgca atgttgatct tctgaagatg atacaactag gcatcacgtt attcaatgac 600
gaaggagagg tccccccagc ctcaggcact gatgccaatg gacaagcgta tggtagtgc 660
gtccctgca catggcagtt caacttccga ttttcacttg aaggcgacat gtacgcccag 720

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```

gagtcaacag ccatgcttgc caaatctgga attgacttgc ccatgcatga aaagaacggc 780
attgatcctt tcgaattcgg tgctcttttg attagctctg gattgggtgct actggatgac 840
gttcaactggg tgtctttcca ctccgggtac gactttggct acttgatgaa gatcatgctc 900
tgctcccagc ttccagaaaa cgaagaggag ttccacaagc ttcttaccat cttcttcccg 960
tcacttttacg acatcaaata cctcatgaag cacgccggtc gcaaccaagc cgtcaacggg 1020
tcccctctca gtcaggctgc agcccagatt ctaccaatc taggccagaa atctggtttg 1080
caagacattg ccgatgaact tggcgtgaag cgcgtcggaa tcgctcacca ggctggctca 1140
gactccctag tcaccggcga gatctactgg aagacgcgcc aactcatttt cggaggggca 1200
attgacgaca gcaaataattc tggccaaatc tggggtctca acggacaaat gcctgcagtg 1260
gcctacaaca tggctcagca aacgcccaac ctaaatggcg cgaccattta ctcgggcggc 1320
acccccagca ctccaatac tgggtctcac ggggtcggcg cccacacacc tcagcactac 1380
ggagctggct acaatgcccc gactcccgga gcctatcaaa tgggccgggt a 1431

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<210> 54

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 54

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Met Pro Pro Pro Val Gly Arg Tyr Ala Pro Ser Gly Leu Asn Ala Pro
 1          5          10          15
Tyr Asn Ile Gln Gln Ala His Leu Gln Ser Gln His Pro Ala His Ala
      20          25          30
Gln Ser Gly Asn Thr Leu Pro Pro Ser Leu Gly His Pro Gly Phe
      35          40          45
Ala Gly Asn Pro Asn Thr Asn Ile Asn Pro Phe Thr Leu Ser Gly Gly
      50          55          60
Ile Ala Asn Gly Met Ala Val Ala Gly Phe Pro Gly Ala Gly Ala Gly
      65          70          75          80
Asp Gly Gly Gly Thr Gly Leu Ala Ser His Ala Ala Gln Met Gly Phe
      85          90          95
Ala Arg Gly Ala Gln Met Gln Gln Gln Gln Leu His Gln Gly His Asp
      100          105          110
Gly Arg Leu Ala Leu Glu Ala Lys Gly Gly Ala Val Lys Ser Arg Ile
      115          120          125
Arg Asp Val Trp Lys His Asn Leu Ala His Glu Met Ala Val Leu Arg
      130          135          140
Gln Leu Val Asp Lys Tyr Pro Tyr Ile Ser Met Asp Thr Glu Phe Pro
      145          150          155          160
Gly Ile Val Ala Arg Pro Ile Gly Ser Phe Ser Asn Lys Ala Asp Tyr
      165          170          175
His Tyr Gln Thr Leu Arg Cys Asn Val Asp Leu Leu Lys Met Ile Gln
      180          185          190
Leu Gly Ile Thr Leu Phe Asn Asp Glu Gly Glu Val Pro Pro Ala Ser
      195          200          205
Gly Thr Asp Ala Asn Gly Gln Ala Tyr Gly Val Pro Ala Pro Cys Thr
      210          215          220
Trp Gln Phe Asn Phe Arg Phe Ser Leu Glu Gly Asp Met Tyr Ala Gln
      225          230          235          240
Glu Ser Thr Ala Met Leu Ala Lys Ser Gly Ile Asp Phe Ala Met His
      245          250          255
Glu Lys Asn Gly Ile Asp Pro Phe Glu Phe Gly Ala Leu Leu Ile Ser
      260          265          270
Ser Gly Leu Val Leu Leu Asp Asp Val His Trp Val Ser Phe His Ser

```

	275					280					285				
Gly	Tyr	Asp	Phe	Gly	Tyr	Leu	Met	Lys	Ile	Met	Leu	Cys	Ser	Gln	Leu
	290					295					300				
Pro	Glu	Asn	Glu	Glu	Glu	Phe	His	Lys	Leu	Leu	Thr	Ile	Phe	Phe	Pro
305					310					315					320
Ser	Leu	Tyr	Asp	Ile	Lys	Tyr	Leu	Met	Lys	His	Ala	Gly	Arg	Asn	Gln
				325					330					335	
Ala	Val	Asn	Gly	Ser	Pro	Leu	Ser	Gln	Ala	Ala	Ala	Gln	Ile	Leu	Thr
			340					345					350		
Asn	Leu	Gly	Gln	Lys	Ser	Gly	Leu	Gln	Asp	Ile	Ala	Asp	Glu	Leu	Gly
		355				360						365			
Val	Lys	Arg	Val	Gly	Ile	Ala	His	Gln	Ala	Gly	Ser	Asp	Ser	Leu	Val
	370					375					380				
Thr	Gly	Glu	Ile	Tyr	Trp	Lys	Thr	Arg	Gln	Leu	Ile	Phe	Gly	Gly	Ala
385					390					395					400
Ile	Asp	Asp	Ser	Lys	Tyr	Ser	Gly	Gln	Ile	Trp	Gly	Leu	Asn	Gly	Gln
				405					410					415	
Met	Pro	Ala	Val	Ala	Tyr	Asn	Met	Ala	Gln	Gln	Thr	Pro	Asn	Leu	Asn
			420					425					430		
Gly	Ala	Thr	Ile	Tyr	Ser	Gly	Gly	Thr	Pro	Ser	Thr	Pro	Asn	Thr	Gly
		435					440					445			
Ser	His	Gly	Ala	Gly	Ala	His	Thr	Pro	Gln	His	Tyr	Gly	Ala	Gly	Tyr
	450					455					460				
Asn	Ala	Pro	Thr	Pro	Gly	Ala	Tyr	Gln	Met	Gly	Arg	Val			
465					470					475					

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<210> 55
<211> 1146
<212> DNA
<213> Artificial Sequence
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<220>  
<223> fungal gene

<400> 55							
atgttttgc	ctggtggaag	ccctcaattt	gcttcgcccc	tgtctggtac	aacacatggg	60	
ttctgggaag	gaaagacggc	cgcccgctcgt	ctttctgtgc	caacgagtag	caaccctttc	120	
ctcgcacagc	atggcaacgc	atatcctcca	ggatatcaca	accccgctcg	tgcaccttat	180	
caaaatgctg	ctggggtatt	cgcaagcccc	actagcacac	actactctgt	atctcgtgat	240	
gagggtagct	taagcgcggc	cgaggcggag	atgctggagga	gaactgtggca	cccttcgtca	300	
taccacagggt	ttccacgccc	tggaactagt	ggcctgaacc	aatatcatac	accgcacaat	360	
gtcccagcct	cattcggtgc	gaacgggtcg	accgagcatc	cgccccggct	tcccggcatt	420	
gagagttttg	acaaggttgt	ccaacggccg	atgaccccg	ccaccaggaa	aaccagccca	480	
atgcagcttg	atggccagca	tcgtccaccc	cctaaccag	gctttggatc	agggttcaat	540	
tatacacagc	cagcccaccg	tccaccaact	cccatctccg	gccctggtca	ccgacgaggc	600	
catgtatcct	gggatattgc	tttgcatcat	aacctgaccg	gcctcgatat	ccgagaccga	660	
cgctccttcta	ccgcattctgc	ttctcaattg	agccaacaaa	ccctcgcaga	actccagaat	720	
gtctcttccc	gcccgtcatc	atcttaacag	cctgcattcg	gccaaccggc	cgagagaagc	780	
ccctaagagt	atcggggaca	tcgccaacg	ctctcaacgg	gaagcgcgac	cgcaacttcc	840	
ccgaagatt	cgagtagcag	cgaggggtgc	cataccccat	ccaccgcac	gcttgagtat	900	
catcccgcga	ttgtgcacag	cagcggatat	atcgaatctg	atgattcctc	cttgcccttc	960	
gatcacccctc	aaccgatctg	tggcgtcag	tcctcccacg	cggatggcta	tgaacccac	1020	
aatgacccggg	agcccaggcc	cgacgtcttc	ccagactctc	ctgcccgaaa	ttcgggcatg	1080	
ggtcgctctgg	aggctcttgt	cgccgtcgcc	acaagcgaga	acaaaggagc	cgccaagcta	1140	
tttctg						1140	

<210> 56  
 <211> 382  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 56  
 Met Phe Ala Ala Gly Gly Ser Pro Gln Phe Ala Ser Pro Met Ser Gly  
 1 5 10 15  
 Thr Thr His Gly Phe Trp Glu Gly Lys Thr Ala Ala Arg Arg Leu Ser  
 20 25 30  
 Val Pro Thr Ser Ser Asn Pro Phe Leu Ala Gln His Gly Asn Ala Tyr  
 35 40 45  
 Pro Pro Gly Tyr His Asn Pro Val Gly Ala Pro Tyr Gln Asn Ala Ala  
 50 55 60  
 Gly Val Phe Ala Ser Pro Thr Ser Thr His Tyr Ser Val Ser Arg Asp  
 65 70 75 80  
 Glu Gly Thr Leu Ser Ala Ala Glu Ala Glu Met Arg Arg Arg Thr Trp  
 85 90 95  
 His Pro Ser Ser Tyr Thr Gly Phe Pro Arg Pro Gly Thr Ser Gly Leu  
 100 105 110  
 Asn Gln Tyr His Thr Pro Asp Asn Val Pro Ala Ser Phe Gly Ala Asn  
 115 120 125  
 Gly Ser Thr Glu His Pro Pro Arg Leu Pro Gly Ile Glu Ser Phe Asp  
 130 135 140  
 Lys Val Val Gln Arg Pro Met Thr Pro Pro Thr Arg Lys Thr Ser Pro  
 145 150 155 160  
 Met Gln Leu Asp Gly Gln His Arg Pro Pro Pro Asn Pro Gly Phe Gly  
 165 170 175  
 Ser Gly Phe Asn Tyr Thr Gln Pro Ala His Arg Pro Pro Pro Pro Ile  
 180 185 190  
 Ser Gly Pro Gly His Arg Arg Gly His Val Ser Trp Asp Met Ser Leu  
 195 200 205  
 His His Asn Leu Thr Gly Leu Asp Ile Arg Asp Arg Arg Pro Ser Thr  
 210 215 220  
 Ala Ser Ala Ser Gln Trp Ser Gln Gln Thr Leu Ala Glu Leu Gln Asn  
 225 230 235 240  
 Val Ser Ser Arg Pro Ser Ser Ser Tyr Gln Pro Ala Phe Gly Pro Thr  
 245 250 255  
 Ala Glu Arg Ser Pro Glu Glu Tyr Arg Gly His Arg Pro Ser Leu Ser  
 260 265 270  
 Thr Gly Ser Arg Thr Arg Thr Ser Pro Glu Asp Ser Ser Ser Ser Glu  
 275 280 285  
 Gly Val His Thr Pro Ser Thr Ala Ser Leu Glu Tyr His Pro Ala Ile  
 290 295 300  
 Val His Ser Ser Gly Tyr Ile Glu Ser Asp Asp Ser Ser Leu Pro Ser  
 305 310 315 320  
 Asp His Pro Gln Pro Ile Cys Gly Arg Gln Ser Ser His Ala Asp Gly  
 325 330 335  
 Tyr Glu Pro His Asn Asp Arg Glu Pro Arg Pro Asp Val Phe Pro Asp  
 340 345 350  
 Ser Pro Ala Arg Asn Ser Gly Met Gly Arg Leu Glu Ala Leu Val Ala  
 355 360 365  
 Val Ala Thr Ser Glu Asn Lys Gly Ala Ala Lys Leu Phe Leu  
 370 375 380

<210> 57  
 <211> 909  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 57  
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 gaggacgtga tgcgcggcat cctcaaccca ccctcgatgg tggattccct acgctttatc 120  
 cgaccccgca ccgaactcac ccagaaacaa agcttccggt ccccgatcga cgagctcgag 180  
 gccaacgccc tggaaaacca ggagccctcc cacgctgctc tatacggata tcgcccgcag 240  
 atgatggccc ctcccacgta cgccatgcc aaccttcaa acgacttcta catgcacccc 300  
 agtccctacg ccgccacaca tccccgcgag caaggccoga tccagggata ctcgatgggc 360  
 gccccgatgg cagcccaaac cgcgccaaac ccatacctgc caagcccagg ccaaaccgcc 420  
 atcccaccga agcaggaaga ctaccacgca ttccgcgcag ggccttatgg cggcagcatg 480  
 gactccatga gcgcacacag catggcctcc atccgggca gcatcaacgc ggggctgtcc 540  
 agctcactca acgaacgaaa cagatccacc tcggatcaca gcccttccgc ttaccgcaat 600  
 tcttccatct cttcgcgcag ccaggccact gacgctactt ccccatgga tccatcaaca 660  
 ccggccacct actccgcgg cagcttcagc atgtccggtc aactggagaa cccacatcca 720  
 gcactogatc gcaacatgcc tgggtctggat gctagcgttc gtcgcgagtc aaatcctatt 780  
 catccgtcct actacactgc ggatcgctcc cagtactatg taccgcgcc ttacgctgcc 840  
 acgcaacctg tgtcgacatg gacgactacg gcggcgacgc aaccacagat ggcgcaacct 900  
 caaatctaa 909

<210> 58  
 <211> 302  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 58  
 Lys Thr Met Ser Val Thr Val Leu Gly Val Thr His His Leu Val Ser  
 1 5 10 15  
 Tyr Tyr Ser Val Glu Asp Val Met Arg Gly Ile Leu Asn Pro Pro Ser  
 20 25 30  
 Met Val Asp Ser Leu Arg Phe Ile Arg Pro Arg Thr Glu Leu Thr Gln  
 35 40 45  
 Lys Gln Ser Phe Arg Ser Pro Ile Asp Glu Leu Glu Ala Asn Ala Val  
 50 55 60  
 Glu Asn Gln Glu Pro Ser His Ala Ala Leu Tyr Gly Tyr Arg Pro Gln  
 65 70 75 80  
 Met Met Ala Pro Pro Thr Tyr Ala Met Pro Thr Pro Ser Asn Asp Phe  
 85 90 95  
 Tyr Met His Pro Ser Pro Tyr Ala Ala Thr His Pro Pro Gln Gln Gly  
 100 105 110  
 Pro Ile Gln Gly Tyr Ser Met Gly Ala Pro Met Ala Ala Gln Thr Ala  
 115 120 125  
 Pro Asn Pro Tyr Leu Pro Ser Pro Gly Gln Thr Ala Ile Pro Pro Lys  
 130 135 140  
 Gln Glu Asp Tyr His Ala Phe Arg Ala Gly Pro Tyr Gly Gly Ser Met  
 145 150 155 160

```

Asp Ser Met Ser Ala His Ser Met Ala Ser Ile Pro Gly Ser Ile Asn
      165      170      175
Ala Gly Leu Ser Ser Leu Asn Glu Arg Asn Arg Ser Thr Ser Asp
      180      185      190
His Ser Pro Ser Ala Tyr Arg Asn Ser Ser Ile Ser Ser Arg Ser Gln
      195      200      205
Ala Thr Asp Ala Thr Ser Pro Met Asp Pro Ser Thr Pro Ala Thr Tyr
      210      215      220
Ser Arg Gly Ser Phe Ser Met Ser Gly Gln Leu Glu Asn Pro His Pro
      225      230      235      240
Ala Leu Asp Arg Asn Met Pro Gly Leu Asp Ala Ser Val Arg Arg Glu
      245      250      255
Ser Asn Pro Ile His Pro Ser Tyr Tyr Thr Ala Asp Arg Ser Gln Tyr
      260      265      270
Tyr Val Pro Ala Pro Tyr Ala Ala Thr Gln Pro Met Ser Thr Trp Thr
      275      280      285
Thr Thr Ala Ala Thr Gln Pro Gln Met Ala Gln Pro Gln Ile
      290      295      300

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<210> 59  
 <211> 918  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 59
atggctccag gcagtgggcg cgactttaac tgctcatggg agcattgtgg aaagtctttc 60
aatcgcaagt cggatctctg tcgccattat cgcattccata ccaatgagcg cccgtatcat 120
tgcaccgtaa aggactgcaa taagagcttc attcagcgga gtgccttgac cgtacactcg 180
aggaccaca ctggcgaaaa gcccatggt tgtgaccatg aaggctgtca gaaggcattc 240
tccgactcat cgagtctagc tcgccatcgc cgaatccaca ccgggaagcg gccatacata 300
tgccacgagc ctacatgcga acggagtttt tgtcgcaaga ccaccctcac caaacaccaa 360
caccgtccc accctccagg gagcttgacc cgaccatcct cagaagatgg gacctccgag 420
cattcttacc accaaacacc cgtatcagtc tcggtcccga ctgagcagta catgctcgcc 480
cagcaacctt tttaccgcga atcggcgaca ccaagtcatg agttttactc gccccaaagt 540
gtgccgatgg gcaccgtgcc ggttcacgaa gctgcccttc cgatcgtggc ccagactgtc 600
cccggaacct cgccggtaaa catgccacac gctcaacagc cgcagccgca cccgcaacac 660
cacgcgcatc cacaacagca gcagcagcag cagcagcagc agcatcaaca atacttacaa 720
atgatgcaac agcgttacga cagtccacgg gcgaactacc tcccagaaca ataccaacat 780
ccatcttttc aaggccacca actgcctccc gaacagccaa tgatgggttc ataccacca 840
aactatgcgt ataaaccccc cggctcccgt ctcttgaacc aagcggaggg gactgactgg 900
ggctttctgg gagtaggc
918

```

<210> 60  
 <211> 306  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 60
Met Ala Pro Gly Ser Gly Arg Asp Phe Asn Cys Ser Trp Glu His Cys
  1           5           10           15

```

Gly Lys Ser Phe Asn Arg Lys Ser Asp Leu Cys Arg His Tyr Arg Ile  
                   20                  25                  30  
 His Thr Asn Glu Arg Pro Tyr His Cys Thr Val Lys Asp Cys Asn Lys  
                   35                  40                  45  
 Ser Phe Ile Gln Arg Ser Ala Leu Thr Val His Ser Arg Thr His Thr  
                   50                  55                  60  
 Gly Glu Lys Pro His Val Cys Asp His Glu Gly Cys Gln Lys Ala Phe  
 65                  70                  75                  80  
 Ser Asp Ser Ser Ser Leu Ala Arg His Arg Arg Ile His Thr Gly Lys  
                   85                  90                  95  
 Arg Pro Tyr Ile Cys His Glu Pro Thr Cys Glu Arg Ser Phe Cys Arg  
                   100                  105                  110  
 Lys Thr Thr Leu Thr Lys His Gln His Arg Ser His Pro Pro Gly Ser  
                   115                  120                  125  
 Leu Thr Arg Pro Ser Ser Glu Asp Gly Thr Ser Glu His Ser Tyr His  
 130                  135                  140  
 Gln Thr Pro Val Ser Val Ser Val Pro Thr Glu Gln Tyr Met Leu Ala  
 145                  150                  155                  160  
 Gln Gln Pro Phe Tyr Pro Gln Ser Ala Thr Pro Ser His Glu Phe Tyr  
                   165                  170                  175  
 Ser Pro Gln Ser Val Pro Met Gly Thr Val Pro Val His Glu Ala Ala  
                   180                  185                  190  
 Pro Pro Ile Val Ala Gln Thr Val Pro Gly Thr Ser Pro Val Asn Met  
                   195                  200                  205  
 Pro His Ala Gln Gln Pro Gln Pro His Pro Gln His His Ala His Pro  
                   210                  215                  220  
 Gln Gln Gln Gln Gln Gln Gln Gln Gln His Gln Gln Tyr Leu Gln  
 225                  230                  235                  240  
 Met Met Gln Gln Arg Tyr Asp Ser Pro Arg Ala Asn Tyr Leu Pro Glu  
                   245                  250                  255  
 Gln Tyr Gln His Pro Ser Phe Gln Gly His Gln Leu Pro Pro Glu Gln  
                   260                  265                  270  
 Pro Met Met Val Ser Tyr His Pro Asn Tyr Ala Tyr Lys Pro Pro Gly  
                   275                  280                  285  
 Ser Arg Leu Leu Asn Gln Ala Glu Gly Thr Asp Trp Gly Phe Leu Gly  
 290                  295                  300  
 Val Gly  
 305

<210> 61  
 <211> 1095  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 61  
 atggataccc attcggatac cgacttgagt catcctcgaa tgcgcgggagc tattgaactg 60  
 ccccgctcc gcgatcattt caagcaggaa tctcttcgc cgtttacgcc tcgtcctcgc 120  
 gagcttcttc catccatcct caatcactcc ccgccgggtc gtcatccac attgccgcca 180  
 atccagcggg gagacaaatt ttcccgcccg cgcaaatctt ccatcactca atctgcgcgg 240  
 aaatccaggc aggatcgccc taaatcaaag gaattcgggc ggcgaccaag tctcggtgac 300  
 cgcaaagccc ttccggcaga gccgcaaacc cgggcctggg cgcaaggcaa gcgctgggag 360  
 gatctgattg aagccgcgac atcagcaacc gaagtagacg atgagccgta ttcagaggct 420  
 ggtcgggtct caacgattgc cccactactt tccaacgtga cgtctgcccc ctctgggggtg 480

```

aaaaatcggg cctcgctacc acccgctttc caatectcgg gattgcctcc tatctcttca 540
catcggccat tcccacctca ttcatacgcc gcctcgccct tgcacaagtc attgacccca 600
ccaccatacg agaaccaccg cagccgtgag agcgacttgg aaccattccc gtctattgaa 660
tcacgcgtcg attccatgtc ttcggcatcc ggcagaaatt ttgcgtcatc ggtttcggga 720
gtcgcgccgt ccataaaactc tgattccage ccagttatga atcttatccc gcccatctcg 780
cagcgccagc accaccgatt ctccaatcct actccagcgt ctttccgcaa caaagagggt 840
caggtgtttt gtgctcagtg caaacgacct tcggcactga atgagtgcta tgctgtacg 900
gagtgcattc gtggagtctg ccgcgactgc gtgagcatgt tcatttcaag tccgcctact 960
tcattccgaa ccccgaggaa cgggtcgtaa aataccgtcc tgtcacaagg accaacaagt 1020
taccctggtc ctcaagggtg tccacgatgt cgaacagttg gaggcaaatt gaaggcattc 1080
caaatcgaca tcaag                                     1095

```

<210> 62

<211> 365

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 62

```

Met Asp Thr His Ser Asp Thr Asp Leu Ser His Pro Arg Met Arg Gly
 1          5          10          15
Ala Ile Glu Leu Pro Pro Leu Arg Asp His Phe Lys Gln Glu Ser Leu
          20          25          30
Pro Pro Phe Thr Pro Arg Pro Arg Glu Leu Leu Pro Ser Ile Leu Asn
          35          40          45
His Ser Pro Pro Gly Arg Ser Ser Thr Leu Pro Pro Ile Gln Arg Arg
          50          55          60
Asp Lys Phe Ser Arg Pro Arg Lys Ser Ser Ile Thr Gln Ser Ala Arg
          65          70          75          80
Lys Ser Arg Gln Asp Arg Pro Lys Ser Lys Glu Phe Gly Arg Arg Pro
          85          90          95
Ser Leu Gly Asp Arg Lys Ala Leu Ser Ala Glu Pro Gln Thr Ala Ala
          100          105          110
Trp Ala Gln Gly Lys Arg Trp Glu Asp Leu Ile Glu Ala Ala Thr Ser
          115          120          125
Ala Thr Glu Val Asp Asp Glu Pro Tyr Ser Glu Ala Gly Arg Ser Pro
          130          135          140
Thr Ile Ala Pro Leu Leu Ser Asn Val Thr Ser Ala Pro Ser Gly Val
          145          150          155          160
Lys Asn Arg Ser Ser Leu Pro Pro Ala Phe Gln Ser Ser Gly Leu Pro
          165          170          175
Pro Ile Ser Ser His Arg Pro Phe Pro Pro His Ser Tyr Ala Ala Ser
          180          185          190
Pro Leu His Lys Ser Leu Thr Pro Pro Pro Tyr Glu Asn His Arg Ser
          195          200          205
Arg Glu Ser Asp Leu Glu Pro Phe Pro Ser Ile Glu Ser Ser Leu Asp
          210          215          220
Ser Met Ser Ser Ala Ser Gly Arg Asn Phe Ala Ser Ser Val Ser Gly
          225          230          235          240
Val Ala Pro Ser Ile Asn Ser Asp Ser Ser Pro Val Met Asn Leu Ile
          245          250          255
Pro Pro Ile Ser Gln Arg Gln His His Arg Phe Ser Asn Pro Thr Pro
          260          265          270
Ala Ser Phe Arg Asn Lys Glu Val Gln Val Phe Cys Ala Gln Cys Lys
          275          280          285

```



```

Arg Pro Ser Ala Leu Asn Glu Cys Tyr Ala Cys Thr Glu Cys Ile Cys
 290                               295                               300
Gly Val Cys Arg Asp Cys Val Ser Met Phe Ile Ser Ser Pro Pro Thr
305                               310                               315                               320
Ser Phe Arg Thr Pro Gly Asn Gly Ser Leu Asn Thr Val Leu Ser Gln
                               325                               330                               335
Gly Pro Thr Ser Tyr Pro Gly Pro Gln Gly Cys Pro Arg Cys Arg Thr
                               340                               345                               350
Val Gly Gly Lys Trp Lys Ala Phe Gln Ile Asp Ile Lys
                               355                               360                               365

```

<210> 63  
 <211> 1197  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 63
atgaagagcg aatcaggtgg ctccggacaac cctgtcaatg cataccctcc tcatgggtcct 60
ccgcccattgc agatggatgc tggacttgcg gattccttct attatgcaca gcccacgggt 120
tcaacccttc gaaacatggc ctatgccctt gcgggatacg ctggcgatcc ccagatgcag 180
caggaacctg tcccgagggg aagagcaggg gttgaaccac cgccaaagac tttccactgc 240
tcaacctgca acaagggtt cgcacggcgc agtgacctg ctgcacatga gcgtattcac 300
accggagtta gacccatgc atgcgagtgg ccgggggtgtg gaaagcagtt cattcaacgc 360
tcggctttaa cagtgcactc ccgtgtacac actggagaga agcctcatat gtgtgagaga 420
tgtggcaagc cttttagcga ctgcctctcg ctggccagac atcgtcgcat tcactccggc 480
aagcgacctt acaaattgcc gtacgccaac tgtcagaaga ccttcacgcg ccgtacgacg 540
ttgacacgcc accaaaacca ccacactggg accatcgaag aagccgctgc tgaaaccgag 600
gcccaattgc ggcaaaataa ggatcgtgga cgtcctggtg aaggaatgtt ctccgagcac 660
gcttccatcc actctacacc gtcaccgcgc cagcatccat ccatgtcacc tgggtggcgag 720
cttccccgcg tgaatatgca tcgtctagct ggcgactact acatgggcac cggtcctatc 780
ccgcctcatg tgctgaggga tttcccccaa ggcagccctc gggtttcccc gactgcgacc 840
tctccttcgc tgtccagcta tggcagtgcg cccacacccc ggcatccat gacctcgcat 900
ccctacgctc cgcctcagcc tcttgaaccc ccggccaaca gtgatcaccg tcccaatagt 960
gtgaacggca gtccacacat gactagtctc ggatgggcct cgcctctca cggtagcatg 1020
ccgtcgcccg gatcgcccaa cgacttcaact taccgagagc ccactggccc tgctgacctg 1080
acatcgatgc cgccacacat gtacttcccc aattctacta ttcgtcggcc taccagcacc 1140
gagccggaga actacgaaat gaagcctcga ggtgaccact catggtccac tgctgta 1197

```

<210> 64  
 <211> 399  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 64
Met Lys Ser Glu Ser Gly Gly Ser Asp Asn Pro Val Asn Ala Tyr Pro
 1           5           10           15
Pro His Gly Pro Pro Pro Met Gln Met Asp Ala Gly Leu Ala Asp Ser
           20           25           30
Phe Tyr Tyr Ala Gln Pro Thr Gly Ser Thr Pro Arg Asn Met Ala Tyr
           35           40           45

```

Ala	Pro	Ala	Gly	Tyr	Ala	Gly	Asp	Pro	Gln	Met	Gln	Gln	Glu	Pro	Val
50						55					60				
Pro	Gln	Gly	Arg	Ala	Gly	Val	Glu	Pro	Pro	Pro	Lys	Thr	Phe	His	Cys
65					70					75					80
Ser	Thr	Cys	Asn	Lys	Gly	Phe	Ala	Arg	Arg	Ser	Asp	Leu	Ala	Arg	His
			85						90					95	
Glu	Arg	Ile	His	Thr	Gly	Val	Arg	Pro	His	Ala	Cys	Glu	Trp	Pro	Gly
			100					105					110		
Cys	Gly	Lys	Gln	Phe	Ile	Gln	Arg	Ser	Ala	Leu	Thr	Val	His	Ser	Arg
		115					120					125			
Val	His	Thr	Gly	Glu	Lys	Pro	His	Met	Cys	Glu	Arg	Cys	Gly	Lys	Pro
		130				135					140				
Phe	Ser	Asp	Ser	Ser	Ser	Leu	Ala	Arg	His	Arg	Arg	Ile	His	Ser	Gly
145					150					155					160
Lys	Arg	Pro	Tyr	Lys	Cys	Pro	Tyr	Ala	Asn	Cys	Gln	Lys	Thr	Phe	Thr
			165						170					175	
Arg	Arg	Thr	Thr	Leu	Thr	Arg	His	Gln	Asn	His	His	Thr	Gly	Thr	Ile
			180					185					190		
Glu	Glu	Ala	Ala	Ala	Glu	Thr	Glu	Ala	Gln	Leu	Arg	Gln	Asn	Lys	Asp
		195					200					205			
Arg	Gly	Arg	Pro	Gly	Glu	Gly	Met	Phe	Ser	Glu	His	Ala	Ser	Ile	His
	210					215					220				
Ser	Thr	Pro	Ser	Pro	Ala	Gln	His	Pro	Ser	Met	Ser	Pro	Gly	Gly	Glu
225					230					235					240
Leu	Pro	Pro	Leu	Asn	Met	His	Arg	Ser	Ala	Gly	Asp	Tyr	Tyr	Met	Gly
			245						250					255	
Thr	Gly	Pro	Ile	Pro	Pro	His	Val	Arg	Gly	Asp	Phe	Pro	Gln	Gly	Ser
		260						265					270		
Pro	Arg	Ala	Ser	Pro	Thr	Ala	Thr	Ser	Pro	Ser	Leu	Ser	Ser	Tyr	Gly
		275				280						285			
Ser	Ala	Pro	His	Thr	Arg	Pro	Ser	Met	Thr	Ser	His	Pro	Tyr	Ala	Pro
	290					295					300				
Pro	Gln	Pro	Leu	Glu	Pro	Pro	Ala	Asn	Ser	Asp	His	Arg	Pro	Asn	Ser
305					310					315					320
Val	Asn	Gly	Ser	Pro	His	Met	Thr	Ser	Leu	Gly	Trp	Ala	Ser	Pro	Ser
			325						330					335	
His	Gly	Ser	Met	Pro	Ser	Pro	Gly	Ser	Ala	Asn	Asp	Phe	Thr	Tyr	Pro
		340						345					350		
Glu	Pro	Thr	Gly	Pro	Ala	Tyr	Pro	Thr	Ser	Met	Pro	Pro	His	Met	Tyr
		355				360						365			
Phe	Pro	Asn	Ser	Thr	Ile	Arg	Arg	Pro	Thr	Ser	Thr	Glu	Pro	Glu	Asn
	370					375					380				
Tyr	Glu	Met	Lys	Pro	Arg	Gly	Asp	His	Ser	Trp	Ser	Thr	Ala	Val	
385					390					395					

&lt;210&gt; 65

&lt;211&gt; 1098

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 65

atgtctaacg caaggcattg ggaacaagat aaagaggcaa ccgtgtacat cggaacacctt 60  
gatgaacggg tctcggacag cctggtatgg gaattgatgc tgcaggttgg ggcgcacgtt 120

```

aacgtccatc tgcccaaaga ccgggtcacg cagttacacc aggggtatgg atttgttgag 180
ttcatcagcg aggaagatgc cgaatatgca tcgaagatca tgaacggaat ccgtctccat 240
ggcaagccta ttcgtgttaa caaggcatcg gctgataagc aaaaaactgt ggaaattggc 300
gctgagctgt ttgtgggtaa tcttgatcct atggttgccg agcaggttct ctttgatacg 360
ttcagccggt ttggcaatct tgtcaatccg cctaaaattg cccgtgatga caacaatctc 420
tctaagggat atggatttgt ttcttttgcc gatttcgaat cctcggacgc ggctatcgcc 480
aacatgaatg gccagtacct gatgaacaaa caggtttctg tacagtatgc atacaagaag 540
gatgggaaag gcgagagaca tggatgatgaa gcagaacgaa tgctggcagc ccaggctcgc 600
aagcataatg cacagccacc cactcagcaa gctccgcagt tccctggcac tggcccgggc 660
gtatcatcaa cgccggccat gtcgaatggc gacatctctc gacccttgag cacagccccg 720
tcacaaacac ccgatgtagg tatgaatcgg ggtgtgacct cagccatggc tccagctatg 780
cctccagctt tgccctacca gagtgcgctt cctccaatgc cttaccagac cgttccccct 840
ccaaaccgac atgtcccacc tcccgctcct tcaactcaata cgccacctcc ggggctccca 900
gctcggcctc cgccttccca agctggctac ggcggccac agaccttttt accacctgga 960
ttcaatggtg caggccaacc gcccttcac cccacaggctg cacctcccc tgggtttggg 1020
ccgcccggat ttggacctcc atctggggcc ccttcattgc caccgggctt ccaacagccc 1080
ggatacggag gcagtcgg                                     1098

```

<210> 66

<211> 366

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 66

```

Met Ser Asn Ala Arg His Trp Glu Gln Asp Lys Glu Ala Thr Val Tyr
 1           5           10           15
Ile Gly Asn Leu Asp Glu Arg Val Ser Asp Ser Leu Val Trp Glu Leu
      20           25           30
Met Leu Gln Val Gly Arg Ile Val Asn Val His Leu Pro Lys Asp Arg
      35           40           45
Val Thr Gln Leu His Gln Gly Tyr Gly Phe Val Glu Phe Ile Ser Glu
      50           55           60
Glu Asp Ala Glu Tyr Ala Ser Lys Ile Met Asn Gly Ile Arg Leu His
65           70           75           80
Gly Lys Pro Ile Arg Val Asn Lys Ala Ser Ala Asp Lys Gln Lys Thr
      85           90           95
Val Glu Ile Gly Ala Glu Leu Phe Val Gly Asn Leu Asp Pro Met Val
      100          105          110
Ala Glu Gln Val Leu Phe Asp Thr Phe Ser Arg Phe Gly Asn Leu Val
      115          120          125
Asn Pro Pro Lys Ile Ala Arg Asp Asp Asn Asn Leu Ser Lys Gly Tyr
      130          135          140
Gly Phe Val Ser Phe Ala Asp Phe Glu Ser Ser Asp Ala Ala Ile Ala
145          150          155          160
Asn Met Asn Gly Gln Tyr Leu Met Asn Lys Gln Val Ser Val Gln Tyr
      165          170          175
Ala Tyr Lys Lys Asp Gly Lys Gly Glu Arg His Gly Asp Glu Ala Glu
      180          185          190
Arg Met Leu Ala Ala Gln Ala Arg Lys His Asn Ala Gln Pro Pro Thr
      195          200          205
Gln Gln Ala Pro Gln Phe Pro Gly Thr Gly Pro Gly Val Ser Ser Thr
      210          215          220
Pro Ala Met Ser Asn Gly Asp Ile Ser Arg Pro Leu Ser Thr Ala Pro
225          230          235          240

```

```

Ser Gln Thr Pro Asp Val Gly Met Asn Arg Gly Val Thr Pro Ala Met
                245                250                255
Ala Pro Ala Met Pro Pro Ala Leu Pro Tyr Gln Ser Ala Pro Pro Pro
                260                265                270
Met Pro Tyr Gln Thr Val Pro Pro Pro Asn Arg His Val Pro Pro Pro
                275                280                285
Val Pro Ser Leu Asn Thr Pro Pro Pro Gly Leu Pro Ala Arg Pro Pro
                290                295                300
Pro Ser Gln Ala Gly Tyr Gly Gly Pro Gln Thr Phe Leu Pro Pro Gly
305                310                315                320
Phe Asn Gly Ala Gly Gln Pro Pro Phe Ile Pro Gln Ala Ala Pro Pro
                325                330                335
Pro Gly Phe Gly Pro Pro Gly Phe Gly Pro Pro Ser Gly Ala Pro Ser
                340                345                350
Leu Pro Pro Gly Phe Gln Gln Pro Gly Tyr Gly Gly Ser Arg
                355                360                365

```

<210> 67  
 <211> 1077  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 67
atggttcttc tcaaaaagca tttgaaagat gtcaaccgtg aggatcagag gcaaattgccg 60
aggcaacggc tgccatctat tcaagaaata tttggggaga cttttctggc gattccttca 120
aatccatcat atgcactgcc ttctcacacc agacatgccg ctccaccggc tttgccggct 180
gtgtatgaaa ttgcccattc aatcgaaggg gctccgtcaa atgagcaagg tttattacc 240
aaaatttcaa cagtggagag atctttgggc attatctctc ccgtcaatga gctccagcat 300
ccggaggtaa tacgcccgga aaatccatcc ttctctccga acggttggtc tcttaacgaa 360
agccgtcgct tttcaaagca cccggaccta tctatacctc aaccgggttt attgtcatgc 420
gatcccatgg atttagcaca gccgtccttt gtcgaaacct caaatgtgtt tcatggattt 480
cccatcagga aaataccaaa ctcgataccg cctcagccaa agcagttatg tctgccggaa 540
aaacgaacac cgagttctct tgatttcagt ctgtttttta aggtgatcga gacagtcagc 600
gcacagacct tggctttcgt gcggtatcac tccgcaatga gtcagtcaga caaccatcaa 660
agatccctcc ctggactatc tatcactgag ataaatggcc tcctcagtca ggagcagcaa 720
aagcaggatg tcttgattta tattagggat gaacttgtgc gcttcgacca ataccaagcc 780
ttagcgcagc agaatactcg ggcagccgca tgtatggcgg gtggggctga ccgaggtctt 840
tgttcacagc tactaaaca gagcaagacc cataaagtct ctaaacaaaa aagagaatgg 900
cacggggata gtgctcttcg ttgtcatagc tgcaaccgtt ctgaaacacc agaatggcgt 960
cgtgggtccg acggccccc aactctttgt aacgcctgtg gtttacatta tgcaaaattg 1020
tctcgacgaa cgggcaaatt tgtggcggtg gacgatattg gcatcagggg caaaaca 1077

```

<210> 68  
 <211> 359  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 68
Met Val Leu Leu Lys Lys His Leu Lys Asp Val Asn Arg Glu Asp Gln
 1             5             10             15

```

```

Arg Gln Met Pro Arg Gln Arg Leu Pro Ser Ile Gln Glu Ile Phe Gly
      20      25      30
Glu Thr Phe Leu Ala Ile Pro Ser Asn Pro Ser Tyr Ala Leu Pro Ser
      35      40      45
His Thr Arg His Ala Ala Pro Pro Ala Leu Pro Ala Val Tyr Glu Ile
      50      55      60
Ala His Ser Ile Glu Gly Ala Pro Ser Asn Glu Gln Gly Leu Leu Pro
      65      70      75      80
Lys Ile Ser Thr Val Glu Arg Ser Leu Gly Ile Ile Ser Pro Val Asn
      85      90      95
Glu Leu Gln His Pro Glu Val Ile Arg Pro Glu Asn Pro Ser Phe Ser
      100      105      110
Pro Asn Gly Cys Ser Leu Asn Glu Ser Arg Arg Phe Ser Lys His Pro
      115      120      125
Asp Leu Ser Ile Pro Gln Pro Gly Leu Leu Ser Cys Asp Pro Met Asp
      130      135      140
Leu Ala Gln Pro Ser Phe Val Glu Pro Pro Asn Val Phe His Gly Phe
      145      150      155      160
Pro Ile Arg Lys Ile Pro Asn Ser Ile Pro Pro Gln Pro Lys Gln Leu
      165      170      175
Cys Leu Pro Glu Lys Arg Thr Pro Ser Ser Leu Asp Phe Ser Leu Phe
      180      185      190
Phe Lys Val Ile Glu Thr Val Ser Ala Gln Thr Leu Ala Phe Val Arg
      195      200      205
Tyr His Ser Ala Met Ser Gln Ser Asp Asn His Gln Arg Ser Leu Pro
      210      215      220
Gly Leu Ser Ile Thr Glu Ile Asn Gly Leu Leu Ser Gln Glu Gln Gln
      225      230      235      240
Lys Gln Asp Val Leu Ile Tyr Ile Arg Asp Glu Leu Val Arg Phe Asp
      245      250      255
Gln Tyr Gln Ala Leu Ala Gln Gln Asn Thr Arg Ala Ala Ala Cys Met
      260      265      270
Ala Gly Gly Ala Asp Arg Gly Leu Cys Ser Ser Val Thr Lys Gln Ser
      275      280      285
Lys Thr His Lys Val Ser Lys Gln Lys Arg Glu Trp His Gly Asp Ser
      290      295      300
Ala Leu Arg Cys His Ser Cys Asn Arg Ser Glu Thr Pro Glu Trp Arg
      305      310      315      320
Arg Gly Pro Asp Gly Pro Arg Thr Leu Cys Asn Ala Cys Gly Leu His
      325      330      335
Tyr Ala Lys Leu Ser Arg Arg Thr Gly Lys Phe Val Ala Leu Asp Asp
      340      345      350
Ile Gly Ile Arg Gly Lys Thr
      355

```

&lt;210&gt; 69

&lt;211&gt; 621

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 69

```

atgtccggct acgaccagta caaccagggt ggctacggcc agcaagggtta tggccagcaa 60
ggttacggcc agccagggtta cggccagcca ggttacgggtg gtcaaccagg ttacgggtggc 120

```

```

caggggtcacg accaacagca acagtagcgtt cagccccaac atgggtacgg ccagcaaggc 180
tacggccagc aggggtggtt ttccgactac tacgccggcc agcaacacca gcagcagggt 240
tacggccagc agcaggggtg ctcttccgac tactacgctg gccagcaaca ccagcagcat 300
gggtacggcc agcacgacca gaaccgtcag ggtggctacg agcagcagca gcatggtgcc 360
cccgatgagg cccaggatgg cgagcgtggt attgctggtg ccctcgcagg tgggtgccgcc 420
ggtggcttcg ctggccacaa ggtcaaccac ggtttccttg gaacaatcgg cggagccatc 480
atcggtagca tcgctgaaga cgccgtcaag aagcaccgca actccgacaa ccagtctcct 540
cctcagtagc gtggccccc tctttccaac agcggcagcg gtgggtccat gatggatcag 600
ctcgggtggt tcttcaagaa g                                     621

```

<210> 70  
 <211> 207  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 70
Met Ser Gly Tyr Asp Gln Tyr Asn Gln Gly Gly Tyr Gly Gln Gln Gly
  1           5           10          15
Tyr Gly Gln Gln Gly Tyr Gly Gln Pro Gly Tyr Gly Gln Pro Gly Tyr
      20           25           30
Gly Gly Gln Pro Gly Tyr Gly Gly Gln Gly His Asp Gln Gln Gln Gln
      35           40           45
Tyr Gly Gln Pro Gln His Gly Tyr Gly Gln Gln Gly Tyr Gly Gln Gln
      50           55           60
Gly Gly Ser Ser Asp Tyr Tyr Ala Gly Gln Gln His Gln Gln Gln Gly
  65           70           75           80
Tyr Gly Gln Gln Gln Gly Gly Ser Ser Asp Tyr Tyr Ala Gly Gln Gln
      85           90           95
His Gln Gln His Gly Tyr Gly Gln His Asp Gln Asn Arg Gln Gly Gly
      100          105          110
Tyr Glu Gln Gln Gln His Gly Ala Pro Asp Glu Ala Gln Asp Gly Glu
      115          120          125
Arg Gly Ile Ala Gly Ala Leu Ala Gly Gly Ala Ala Gly Gly Phe Ala
      130          135          140
Gly His Lys Val Asn His Gly Phe Leu Gly Thr Ile Gly Gly Ala Ile
  145          150          155          160
Ile Gly Ser Ile Ala Glu Asp Ala Val Lys Lys His Arg Asn Ser Asp
      165          170          175
Asn Gln Ser Pro Pro Gln Tyr Gly Gly Pro Pro Pro Ser Asn Ser Gly
      180          185          190
Ser Gly Gly Ser Met Met Asp Gln Leu Gly Gly Phe Phe Lys Lys
      195          200          205

```

<210> 71  
 <211> 789  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

```

<400> 71
atgtcgcacc tgggtgcaat tacctcccc gaccggaggt tcaattcaga tgcccagagaa 60

```

```

ttcttcactc gtcatatgag aattctcag acatgctccg ccgcctggcc catgccggag 120
attcaggctc agatcgattc attaagactg gctttctccg ccgatatgca gcgtcctttc 180
gagttgaagc ccagtttccc atacggcagt cctcgggaac cctaccatcc cagtccacct 240
atggatgcgc actaccatcc gcacttgaat caaatccaat ccagagtgcg ttacaaccgc 300
ctccccgcaa cccctccgat ttccgctggg gctgaagatt cgaagtccga cacatcttcc 360
cagatacaat cctcgggat ggttgcccat cagccttcaa caactcatcc tctagatgcc 420
ccttcggtcg atgaaaatca ctgggacccg acccgaatca tcaactcaatg ggacatggcc 480
ttctccgtga acccttctac cgtcagcaca aactccccac caatgcctat aaacaattca 540
gtaccgagtg taaaaaacgt tatgaacccc caatacccta tccaatacga gacacccaac 600
aaagtgcctt ctgtcacatc taccactct ctctcgctt cgcagttcca gacacctcca 660
gttgtgtttt cagcacgaga ctggcagcaa agtgttgcca gtgtgtatga tccacaaggg 720
ctgaaacggc gatggaatta tccagttgat gctagctccg acaataatat gtccaagcgc 780
caaagagga 789

```

<210> 72

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 72

```

Met Leu His Leu Val Ala Ile Thr Ser Pro Asp Pro Glu Phe Asn Ser
 1             5             10             15
Asp Ala Arg Glu Phe Phe Thr Arg His Met Arg Ile Leu Glu Thr Cys
      20             25             30
Ser Ala Ala Trp Pro Met Pro Glu Ile Gln Ala Gln Ile Asp Ser Leu
      35             40             45
Arg Leu Ala Phe Ser Ala Asp Met Gln Arg Pro Phe Glu Leu Lys Pro
      50             55             60
Ser Phe Pro Tyr Gly Ser Pro Ser Glu Pro Tyr His Pro Ser Pro Pro
      65             70             75             80
Met Asp Ala His Tyr His Pro His Leu Asn Gln Ile Gln Ser Arg Val
      85             90             95
Arg Tyr Asn Pro Leu Pro Ala Thr Pro Pro Ile Ser Ala Gly Ala Glu
      100            105            110
Asp Ser Lys Ser Asp Thr Ser Ser Gln Ile Gln Ser Leu Gly Met Val
      115            120            125
Ala His Gln Pro Ser Thr Thr His Pro Leu Asp Ala Pro Ser Val Asp
      130            135            140
Glu Asn His Trp Asp Pro Thr Arg Ile Ile Thr Gln Trp Asp Met Ala
      145            150            155            160
Phe Ser Val Asn Pro Ser Thr Val Ser Thr Asn Ser Pro Pro Met Pro
      165            170            175
Ile Asn Asn Ser Val Pro Ser Val Gln Asn Val Met Asn Pro Gln Tyr
      180            185            190
Pro Ile Gln Tyr Glu Thr Pro Asn Lys Val Pro Ser Val Thr Ser Thr
      195            200            205
His Ser Leu Ser Pro Ser Gln Phe Gln Thr Pro Pro Val Val Phe Ser
      210            215            220
Ala Arg Asp Trp Gln Gln Ser Val Ala Ser Val Tyr Asp Pro Gln Gly
      225            230            235            240
Leu Lys Arg Arg Trp Asn Tyr Pro Val Asp Ala Ser Ser Asp Asn Asn
      245            250            255
Met Ser Lys Arg Gln Arg Gly
      260

```

<210> 73  
 <211> 2745  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 73  
 atggagccca acgaactttc cttcctgctc aagatggtcc agcgaacctc acaagagggc 60  
 cagccccggg caaacggcat cagcgatgtc gcaaccccggt atataggctc cgcacccgag 120  
 cacatcatgt cgttcgatat caaggatgtc gtcgacattg ccgttcctaaa cgttaccaca 180  
 gctgaagttt cagccaagga accaaacggt gcttcccagg gtttcaggac agacagtgat 240  
 atctccggaa acctagccat gcgagaacgc accttgcagc gctgggaacc ggctgagact 300  
 gacattgata tgtcactcga aacgagcaat acttctgcgg gatgggatca gtttgaggca 360  
 aacgagcgtc ttttcggcgc caagaccaac tacgatgaga acatctacac cactcgccgtg 420  
 gaccgttcgg atcccaacta caaacagaag caggcggagg cagctcggat cgcccgtag 480  
 attgagggac aagatgtgga caactccac atgcgcgagg agcgtggcct tgtagcacc 540  
 gataccggtg accaagacga agaagacaag tacagtgtgt ttcgccgca agacaaagcc 600  
 ttccctcccc tgttttcgg ccagccaaac aagtacatgc ccccgagac cgcacaggca 660  
 gccccacagt ctactgcgac tcccagtga tccaccaaac agcctgttgc tccggttccc 720  
 accgctccta tccccatccc ctctcaggcc gtggcgagg aaactacacc agcagaccag 780  
 caaactgagc tggtcgcctc tctgcaaccc acaacagata ccgagcagaa gagtgcctta 840  
 ggcaagggtg tcacaccgcc agtatctact gcatcccccg caccagctgg aaagcggact 900  
 gcacctgaaa atgcgaccgc aaacgtggag gtggagggtc ttgatcactt ccggcagttc 960  
 gcaaatagcg agaaaatcaa gatgcaggag cgccgtcgca accaggcctc gtatgaccgg 1020  
 accatgaaac tcaatgagct gatgaagttt tccaagagct tcaaactctc cactccggtg 1080  
 ccgaaagatc ttgttctat cctagccaa gaccgactaa agcaagaagc aatcatgcaa 1140  
 cgagcgtgc aacaagggga cgacaaggct acgccgaagg tcaactacgc tcccacagag 1200  
 caacaaccgc ctactcgtgg tgccggacct agtgaggctg tgcccccatc cgcacccgct 1260  
 gatcgtcaaa actacaaccg cactcgtcag ggttatcctc cagctggtcc gctcgttgt 1320  
 gctggtggca gattccctca gcaagttcca ccgggacgtc ctggtgttg catgctcagt 1380  
 caccgactag cggacaatct gcagcaacga aagggcgcg gtatgggacc tgttcccact 1440  
 cctcttccca ttcaagatgc ccgtggacct ccgactggtc ctgccagca tcagcagaga 1500  
 atcaccagcc ctgtcaagtc gcaggccgg tcttctcgcg caaccaagtt taatgttaaa 1560  
 gctatggagt tcaagccaaa ccccgagcg agcactttca cccctggtac ctcgggaaact 1620  
 gccgcaagcc cacggccttt ctctcgcaac cgctccgtgt cacgcgccac aaccccgact 1680  
 gcgttctttg gctcaaggaa gccactgct gtctccgaac gaccctcgat cagtgaacca 1740  
 ttcaatccca tcaagcgcag gaagaaggag cacgcagaga ccgctgagag gttgattatg 1800  
 ctgaatggag gtatcccccc accctacaag actttgccaa cttgggacat cgcggacggc 1860  
 agcgaagaga agacgtacga tgagatgttc aaacagcccg tcgccgttcc cacagtacca 1920  
 ccccagggtc ggtccgtctc taacaacacc aatattcccc agcaacatca ggtgcccttc 1980  
 cacttccagc aagtaaccc agccatgcc ccattctctg gcccttcgaa tggacctcat 2040  
 ggcccttcatt ctgagggtcc ccattggccc tcccattgtg atgatcatca ccgcatgcag 2100  
 ttatccgctc cgaactccca ggttttcccg tcccccgga tgcaacatgg ataccatcc 2160  
 cctatggctc ccatgccca gctttccttc ccacaacgg tcccgcagtt ttacggcggg 2220  
 ccccaacctg gccatatcag acctttccag ggtggtggtc ctcagtttgt gaatggcgt 2280  
 cctatgatgg tgcagaggc ctgcaatgga ccctacatgg gagtcccga aggcattgtc 2340  
 ccctataacg cacagatgcc aatgtactcc ccgaacccag gccacgccta tccccaat 2400  
 acaccccgag ctcatagtgg gtacccaagc ccgagccgtg gtgcgccat gatgatgcac 2460  
 cagaactcgc aatctggaca gcctcctcaa tcaatgatgt ttatgcccg ccaacccggt 2520  
 taccctcagc agtcgggaca catgcctccc aaccgtggca actaccaca gcagcctcac 2580  
 ttttctccta gtcccatca atcgcatcat ttcccaacta accagcatcg gacaccagc 2640  
 aacggtttca accaaatgcc tcaaatgcca cccagatgc ctgccgtac cccagcaaca 2700  
 acccctggag cttctcacc ggccgaggca acggatgaag gaaaa 2745



<210> 74  
 <211> 915  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 74

Met	Glu	Pro	Asn	Glu	Leu	Ser	Phe	Leu	Leu	Lys	Met	Val	Gln	Arg	Thr
1				5					10					15	
Ser	Gln	Glu	Gly	Gln	Pro	Arg	Ala	Asn	Gly	Ile	Ser	Asp	Val	Ala	Thr
			20					25					30		
Pro	Tyr	Ile	Gly	Ser	Ala	Pro	Glu	His	Ile	Met	Ser	Phe	Asp	Ile	Lys
		35					40					45			
Asp	Val	Val	Asp	Ile	Ala	Val	Pro	Asn	Val	Thr	Thr	Ala	Glu	Val	Ser
	50					55					60				
Ala	Lys	Glu	Pro	Asn	Gly	Ala	Ser	Gln	Gly	Phe	Arg	Thr	Asp	Ser	Asp
65				70					75					80	
Ile	Ser	Gly	Asn	Leu	Ala	Met	Arg	Glu	Arg	Thr	Leu	Gln	Arg	Trp	Glu
			85					90					95		
Pro	Ala	Glu	Thr	Asp	Ile	Asp	Met	Ser	Leu	Glu	Thr	Ser	Asn	Thr	Ser
			100				105						110		
Ala	Gly	Trp	Asp	Gln	Phe	Glu	Ala	Asn	Glu	Arg	Leu	Phe	Gly	Ala	Lys
		115				120						125			
Thr	Asn	Tyr	Asp	Glu	Asn	Ile	Tyr	Thr	Thr	Arg	Leu	Asp	Arg	Ser	Asp
	130					135					140				
Pro	Asn	Tyr	Lys	Gln	Lys	Gln	Ala	Glu	Ala	Ala	Arg	Ile	Ala	Arg	Glu
145				150					155					160	
Ile	Glu	Gly	Gln	Asp	Val	Asp	Asn	Ser	His	Met	Arg	Glu	Glu	Arg	Gly
			165					170					175		
Leu	Val	Ala	Pro	Asp	Thr	Gly	Asp	Gln	Asp	Glu	Glu	Asp	Lys	Tyr	Ser
		180					185						190		
Gly	Val	Arg	Arg	Glu	Asp	Lys	Ala	Phe	Pro	Pro	Leu	Leu	Ser	Gly	Gln
		195				200						205			
Pro	Asn	Lys	Tyr	Met	Pro	Pro	Gly	Arg	Arg	Gln	Ala	Ala	Pro	Gln	Ser
	210					215				220					
Thr	Ala	Thr	Pro	Ser	Ala	Ser	Thr	Lys	Gln	Pro	Val	Ala	Pro	Val	Pro
225				230					235					240	
Thr	Ala	Pro	Ile	Pro	Ile	Pro	Ser	Gln	Ala	Val	Ala	Lys	Glu	Thr	Thr
			245					250					255		
Pro	Ala	Asp	Gln	Gln	Thr	Glu	Leu	Val	Ala	Ser	Leu	Gln	Pro	Thr	Thr
		260					265						270		
Asp	Thr	Glu	Gln	Lys	Ser	Ala	Leu	Gly	Lys	Gly	Val	Thr	Pro	Pro	Val
	275						280					285			
Ser	Thr	Ala	Ser	Pro	Ala	Pro	Ala	Gly	Lys	Arg	Thr	Ala	Pro	Glu	Asn
	290				295						300				
Ala	Thr	Ala	Asn	Val	Glu	Val	Glu	Val	Leu	Asp	His	Phe	Arg	Gln	Phe
305				310					315					320	
Ala	Asn	Ser	Glu	Lys	Ile	Lys	Met	Gln	Glu	Arg	Arg	Arg	Asn	Gln	Ala
			325					330					335		
Ser	Tyr	Asp	Arg	Thr	Met	Lys	Leu	Asn	Glu	Leu	Met	Lys	Phe	Ser	Lys
		340					345					350			
Ser	Phe	Lys	Leu	Ser	Thr	Pro	Val	Pro	Lys	Asp	Leu	Val	Pro	Ile	Leu
	355					360					365				
Ala	Lys	Asp	Arg	Leu	Lys	Gln	Glu	Ala	Ile	Met	Gln	Arg	Ala	Leu	Gln

370		375		380
Gln Gly Asp Asp Lys Ala Thr Pro Lys Val Thr Thr Pro Pro Thr Glu				
385		390		400
Gln Gln Pro Pro Thr Arg Gly Ala Gly Pro Ser Gly Ala Val Pro Pro				
	405		410	415
Ser Ala Pro Ala Asp Arg Gln Asn Tyr Asn Arg Thr Arg Gln Gly Tyr				
	420		425	430
Pro Pro Ala Gly Pro Leu Ala Gly Ala Gly Gly Arg Phe Pro Gln Gln				
	435		440	445
Val Pro Pro Gly Arg Pro Gly Val Gly Met Leu Ser His Arg Leu Ala				
	450		455	460
Asp Asn Leu Gln Gln Arg Lys Gly Ala Gly Met Gly Pro Val Pro Thr				
465		470		480
Pro Leu Pro Ile Gln Asp Ala Arg Gly Pro Pro Thr Gly Pro Ala Ser				
	485		490	495
Asp Gln Gln Arg Ile Thr Ser Pro Val Lys Ser Gln Ala Gly Ser Ser				
	500		505	510
Ala Ala Thr Lys Phe Asn Val Lys Ala Met Glu Phe Lys Pro Asn Pro				
	515		520	525
Ala Ala Ser Thr Phe Thr Pro Gly Thr Ser Gly Thr Ala Ala Ser Pro				
	530		535	540
Arg Pro Phe Ser Arg Asn Arg Ser Val Ser Arg Ala Thr Thr Pro Thr				
545		550		560
Ala Phe Phe Gly Ser Arg Lys Pro Leu Pro Val Ser Glu Arg Pro Ser				
	565		570	575
Ile Ser Asp Gln Phe Asn Pro Ile Lys Arg Met Lys Lys Glu His Ala				
	580		585	590
Glu Thr Ala Glu Arg Leu Ile Met Leu Asn Gly Gly Ile Pro Pro Pro				
	595		600	605
Tyr Lys Thr Leu Pro Thr Trp Asp Ile Ala Asp Gly Ser Glu Glu Lys				
	610		615	620
Thr Tyr Asp Glu Met Phe Lys Gln Pro Val Ala Val Pro Thr Val Pro				
625		630		640
Pro Gln Gly Arg Ser Val Ser Asn Asn Thr Asn Ile Pro Gln Gln His				
	645		650	655
Gln Val Pro Phe His Phe Gln Gln Gly Asn Pro Ala Met Pro Pro Ser				
	660		665	670
Ser Gly Pro Ser Asn Gly Pro His Gly Leu His Ser Gln Gly Pro His				
	675		680	685
Gly Pro Ser His Val Asp Asp His His Arg Met Gln Leu Ser Ala Ser				
	690		695	700
Asn Ser Gln Val Phe Pro Ser Pro Arg Met Gln His Gly Tyr Pro Ser				
705		710		720
Pro Met Ala Pro His Ala Gln Leu Ser Phe Pro Gln Pro Val Pro Gln				
	725		730	735
Phe Tyr Gly Gly Pro Gln Pro Gly His Ile Arg Pro Phe Gln Gly Gly				
	740		745	750
Gly Pro Gln Phe Val Asn Gly Ala Pro Met Met Val Gln Gln Ala Ser				
	755		760	765
Asn Gly Pro Tyr Met Gly Val Pro Gln Gly Met Ser Pro Tyr Asn Ala				
	770		775	780
Gln Met Pro Met Tyr Ser Pro Asn Pro Gly His Ala Tyr Pro Gln His				
785		790		800
Thr Pro Gln Pro His Ser Gly Tyr Pro Ser Pro Ser Arg Gly Ala Pro				
	805		810	815
Met Met Met His Gln Asn Ser Gln Ser Gly Gln Pro Pro Gln Ser Met				
	820		825	830

Met Phe Met Pro Gly Gln Pro Gly Tyr Pro Gln Gln Ser Gly His Met  
           835                          840                          845  
 Pro Pro Asn Arg Gly Asn Tyr Pro Gln Gln Pro His Phe Ser Ser Ser  
       850                          855                          860  
 Pro His Gln Ser His His Phe Pro Pro Asn Gln His Arg Thr Pro Ser  
 865                          870                          875                          880  
 Asn Gly Phe Asn Gln Met Pro Gln Met Pro Pro Gln Met Pro Ala Ala  
                           885                          890                          895  
 Thr Pro Ala Thr Thr Pro Gly Ala Ser His Pro Ala Glu Ala Thr Asp  
           900                          905                          910  
 Glu Gly Lys  
           915

<210> 75  
 <211> 1470  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 75  
 atgggttttg ctcagaaaat cgccgcagct cagaatagcc agaacatggc taacagtggg 60  
 tcatatggag gtgcacctcc gtcaggatac actgggggtc ctctgcccgc tctgcagcct 120  
 ggtggatoga gccaacagcc ccaataccag gcttattcag gatccccagc ccccagggga 180  
 tcggcaccac cctaccctac ccagggttcc ccgtaccccc gtggccaggg ccgtcctggg 240  
 ccctcaccag gaccaccaag cggaccgccc ccaggccaat atggcgccacc cgggtggcgcc 300  
 cctccctccg catctcccc ggccactcag caacagggtcg cagcctaccg atcgcttttg 360  
 atttccgcga ttcaggagaa gaacctccaa agcttctacc ctcccagcg actggaccga 420  
 ctcgttcagt cgcttgccgc tgaagcacca ggcaagctca ataggctgat tcatgaatgg 480  
 gccgtgccta tggaggttgc gaccgatgtc atgaagcttt cgctgtttga cgtggttctc 540  
 tatgttgatg acagtggatc tatcgaattc gaagagaagg gactccgaaa ggaccagctc 600  
 aaacaaattc tcggcatcgt agctactgcc gcatctacct ttgaccagga tggatattct 660  
 gtccgattca tgaactccag cgagaagggc gatggcatcc gcaatgcaga ggatgtcgag 720  
 cgcttagtgt cccgagtcgg tttttcaggc ctgacccctc tgggcaccag tctgaggagc 780  
 aaagtcatcg accccatggg tgttcaacct gccaggcca accgtctcga caagcccgtt 840  
 ctggtgatca ccatcaccga cggacagcct gctggcgagc ctcatggtac cgtgggtgat 900  
 gtcatcgcgt acgcagtgga ggagacgtca cggacccgtt atggccccgg caccgtagcc 960  
 ttccagttct cgcagggtgg aactgatcag cgggctcgcg acttcttggg ctctctggat 1020  
 gaggaccctc atatcggccca tctgatcgac tgtacttcca actttgaggt tgagcaggat 1080  
 gagatgtcgc gtgctaacct acccgtgcat ctactcgcg agctttggtg ccccaaactg 1140  
 atgctcggcg ctatcgattc ttcttacgac accaaggatg agcgagagaa tcaacgtcgt 1200  
 ggtgcacccc caccaacagg ccagtacgga ggagggtacg gccaacctcc gccaccccag 1260  
 ggccaagctc agcctccgta tggtcgccc cctggtgccc caccggcttc gtacggttct 1320  
 cagccagggt acccaccgca gggccaatac caacagcctc cccagcagcc tccctaccag 1380  
 ggatcgcggg gtgggtatgg ccaacagcag ccacatgggt atggatcccc tggacctggc 1440  
 taccagtatg gtggacagcc gccacgctat 1470

<210> 76  
 <211> 490  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

&lt;400&gt; 76

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Met Gly Phe Ala Gln Lys Ile Ala Ala Ala Gln Asn Ser Gln Asn Met
1      5      10      15
Ala Asn Ser Gly Ser Tyr Gly Gly Ala Pro Pro Ser Gly Tyr Thr Gly
20      25      30
Gly Pro Pro Ala Ala Leu Gln Pro Gly Gly Ser Ser Gln Gln Pro Gln
35      40      45
Tyr Gln Ala Tyr Ser Gly Ser Pro Ala Pro Gln Gly Ser Ala Pro Pro
50      55      60
Tyr Pro Thr Gln Gly Ser Pro Tyr Pro Gly Gly Gln Gly Arg Pro Gly
65      70      75      80
Pro Ser Pro Gly Pro Pro Ser Gly Pro Pro Pro Gly Gln Tyr Gly Ala
85      90      95
Pro Gly Gly Ala Pro Pro Ser Ala Ser Pro Pro Ala Thr Gln Gln Gln
100     105     110
Val Ala Ala Tyr Arg Ser Leu Leu Ile Ser Ala Ile Gln Glu Lys Asn
115     120     125
Leu Gln Ser Phe Tyr Pro Pro Glu Arg Leu Asp Arg Leu Val Gln Ser
130     135     140
Leu Ala Ala Glu Ala Pro Gly Lys Leu Asn Arg Leu Ile His Glu Trp
145     150     155     160
Ala Val Pro Met Glu Val Ala Thr Asp Val Met Lys Leu Ser Leu Phe
165     170     175
Asp Val Val Leu Tyr Val Asp Asp Ser Gly Ser Ile Glu Phe Glu Glu
180     185     190
Lys Gly Leu Arg Lys Asp Gln Leu Lys Gln Ile Leu Gly Ile Val Ala
195     200     205
Thr Ala Ala Ser Thr Phe Asp Gln Asp Gly Ile Ser Val Arg Phe Met
210     215     220
Asn Ser Ser Glu Lys Gly Asp Gly Ile Arg Asn Ala Glu Asp Val Glu
225     230     235     240
Arg Leu Val Ser Arg Val Arg Phe Ser Gly Leu Thr Pro Leu Gly Thr
245     250     255
Ser Leu Arg Ser Lys Val Ile Asp Pro Met Val Val Gln Pro Ala Gln
260     265     270
Ala Asn Arg Leu Asp Lys Pro Val Leu Val Ile Thr Ile Thr Asp Gly
275     280     285
Gln Pro Ala Gly Glu Pro His Gly Thr Val Gly Asp Val Ile Arg Tyr
290     295     300
Ala Val Glu Glu Thr Ser Arg Thr Arg Tyr Gly Pro Gly Thr Val Ala
305     310     315     320
Phe Gln Phe Ser Gln Val Gly Thr Asp Gln Arg Ala Arg Asp Phe Leu
325     330     335
Gly Ser Leu Asp Glu Asp Pro His Ile Gly His Leu Ile Asp Cys Thr
340     345     350
Ser Asn Phe Glu Val Glu Gln Asp Glu Met Ser Arg Ala Asn Pro Pro
355     360     365
Val His Leu Thr Arg Glu Leu Trp Cys Pro Lys Leu Met Leu Gly Ala
370     375     380
Ile Asp Ser Ser Tyr Asp Thr Lys Asp Glu Arg Glu Asn Gln Arg Arg
385     390     395     400
Gly Ala Pro Pro Pro Thr Gly Gln Tyr Gly Gly Gly Tyr Gly Gln Pro
405     410     415
Pro Pro Pro Gln Gly Gln Ala Gln Pro Pro Tyr Gly Pro Pro Pro Gly
420     425     430
Ala Pro Pro Ala Ser Tyr Gly Ser Gln Pro Gly Tyr Pro Pro Gln Gly
435     440     445

```

Gln Tyr Gln Gln Pro Pro Gln Gln Pro Pro Tyr Gln Gly Ser Arg Gly  
 450 455 460  
 Gly Tyr Gly Gln Gln Gln Pro His Gly Tyr Gly Ser Pro Gly Pro Gly  
 465 470 475 480  
 Tyr Gln Tyr Gly Gly Gln Pro Pro Arg Tyr  
 485 490

<210> 77  
 <211> 1215  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 77  
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 agcaaaatga tcgccttgga ttcgteccgc cagcagcaga cccattctt ccagaatttc 120  
 accatggatc ctgcattcac ggaccctttc gcattccagg tggacacctt cgctagcttc 180  
 ggacagcccg ccagttcctc tcgaggcccc cagacttcat attatgatac ccctccgctc 240  
 tacacggatt cttactccga ctccaataag accgcccctg ggtttccttc catgccgggt 300  
 acgccccga cgcttccttc caccagccg ctggactccc acgttcctgg cctgaccgcc 360  
 ccgtcgggtc cgtctgtcgc cagcgccctc tcctcggcca ttgggtcgcc gtactccggc 420  
 acggcccatg ccaaccagga gaactgggtc gatacgaacc acggcctggg ccttcccgcc 480  
 gcggtgatgg gggatctgtt tccgaacgac tacacgggga cgaccctgga ccccgattac 540  
 ttgccaata aaggcgcgga cagctttgtt gacccttctt tgatcccgtt tcagcagcag 600  
 tcgaatctgt cgaccccggc catctcctac ccggaacaga ctgattatag cctgggtccc 660  
 ggcggtattc tccctcagtc cctgaccct tccaattcc aatttgcgga cccctatggt 720  
 ccattcacac agcagccatg ccccatgccc gcctcatccc catctctgat gccctcccat 780  
 gtcccgcccc gtctgtcttc cctctacgac cgtcggctct cggctctctc cgtgcagtcc 840  
 cgtcgtctgc agctgagccc ggcgccagc aacgccgaga tcgaggagga cgccaaggaa 900  
 aagggccgat gccctcatcc ggattgcggt cgagtcttcc gggacctgaa agcgcatatg 960  
 ctgacgcata agtcggagcg tccggagaaa tgcccattg tcacttgca gtaccacacc 1020  
 aagggtttg cccgcaagta cgacaagaac cgccacaccc tgaccacta caagggaacg 1080  
 atggtttgcg gcttctgccc gggatccggg tcgccggccg agaagagctt caaccgggcg 1140  
 gatgtgtca aacgtcatct gacctctgtg cacggtgtgg aacagacccc tcccaactgc 1200  
 cggaaagagaa gcccc 1215

<210> 78  
 <211> 405  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 78  
 Met Gln Ser Pro Gln Gln Pro Pro Asp Phe Leu Leu Tyr Pro Thr Gln  
 1 5 10 15  
 Ser Thr Arg Gly Ser Lys Met Ile Ala Leu Asp Ser Ser Arg Gln Gln  
 20 25 30  
 Gln Thr Pro Phe Phe Gln Asn Phe Thr Met Asp Pro Ala Phe Thr Asp  
 35 40 45  
 Pro Phe Ala Phe Gln Val Asp Thr Phe Ala Ser Phe Gly Gln Pro Ala  
 50 55 60  
 Ser Ser Ser Arg Gly Pro Gln Thr Ser Tyr Tyr Asp Thr Pro Pro Leu

```

65          70          75          80
Tyr Thr Asp Ser Tyr Ser Asp Ser Asn Lys Thr Ala Pro Gly Phe Pro
      85          90          95
Ser Met Pro Gly Thr Pro Pro Thr Leu Pro Ser Thr Gln Pro Leu Asp
      100        105        110
Ser His Val Pro Gly Leu Thr Ala Pro Ser Gly Pro Ser Val Ala Ser
      115        120        125
Ala Ser Ser Ser Ala Ile Gly Ser Pro Tyr Ser Gly Thr Ala His Ala
      130        135        140
Asn Gln Glu Asn Trp Val Asp Thr Asn His Gly Leu Gly Leu Pro Ala
145          150        155        160
Ala Val Met Gly Asp Leu Phe Pro Asn Asp Tyr Thr Gly Thr Thr Leu
      165        170        175
Asp Pro Asp Tyr Phe Ala Asn Lys Gly Ala Asp Ser Phe Val Asp Pro
      180        185        190
Ser Leu Ile Pro Leu Gln Gln Gln Ser Asn Leu Ser Thr Pro Ala Ile
      195        200        205
Ser Tyr Pro Glu Gln Thr Asp Tyr Ser Leu Val Pro Gly Gly Phe Phe
      210        215        220
Pro Gln Ser Pro Asp Pro Ser Gln Phe Gln Phe Ala Asp Pro Tyr Gly
225          230        235        240
Pro Phe Thr Gln Gln Pro Cys Pro Met Pro Ala Ser Ser Pro Ser Leu
      245        250        255
Met Pro Ser His Val Pro Pro Arg Arg Leu Ser Leu Tyr Asp Arg Arg
      260        265        270
Ser Ser Val Ser Ser Val Gln Ser Arg Arg Ser Gln Leu Ser Pro Ala
      275        280        285
Ala Ser Asn Ala Glu Ile Glu Glu Asp Ala Lys Glu Lys Gly Arg Cys
      290        295        300
Pro His Pro Asp Cys Gly Arg Val Phe Arg Asp Leu Lys Ala His Met
305          310        315        320
Leu Thr His Gln Ser Glu Arg Pro Glu Lys Cys Pro Ile Val Thr Cys
      325        330        335
Glu Tyr His Thr Lys Gly Phe Ala Arg Lys Tyr Asp Lys Asn Arg His
      340        345        350
Thr Leu Thr His Tyr Lys Gly Thr Met Val Cys Gly Phe Cys Pro Gly
      355        360        365
Ser Gly Ser Pro Ala Glu Lys Ser Phe Asn Arg Ala Asp Val Phe Lys
      370        375        380
Arg His Leu Thr Ser Val His Gly Val Glu Gln Thr Pro Pro Asn Cys
385          390        395        400
Arg Lys Arg Ser Pro
      405

```

```

<210> 79
<211> 1389
<212> DNA
<213> Artificial Sequence

```

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<220>
<223> fungal gene

```

```

<400> 79
atggagacgt actacggcca tgtccgcact cctgcggacg ccatcatcct cttcgaggcc 60
tgtcgcatgt gtcttctccc tcgctccag cgctcgactgt ccgagaaaga acggcagttg 120
atccgctctg ggtccgtctt tgtctgggat gagcgagaag ccggcatgcg ccgctggacg 180

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gacggcaagt cctggagcgc cagtcgcgtg tctggcagct ttctcacgta tcgcgagatg 240
gaaggcaagc gaggaggcac cggagtatcg cagagcacca ttccgcgagc cgggaaaact 300
cccgagagca cccgcggcag tgacgacgac cgcggcgatg gcgcagacga aggccccgat 360
ggctaccgat ataagcccga cggcttgatg aagcagtcct tcagtatcac cacctccgcc 420
ggccaacacc tccatctcat cagctactac tcgcgtccc atccgtccgc cgccaacctg 480
caacagccca ccaacgatcc caccctgcgc catgttcgac ccagaaagg cctctatccc 540
gaatccacgg tcaacgacca gcagaacctg cccgtcgtga ctgcgcgccc catgggcggt 600
gcttactccg tccaccaccc catgcctccc tacgctcgct ccggcgccac gcatccgcaa 660
tcatacactc cgccctatgc ctggcccccg acgcgcgtgg ccaccccgcc cgtcaccgtc 720
cattactcgc catacctccc gccggtgtcg ggcccaacg gccaactcta cgctcatcat 780
catcaacccc cgcacgcggg gctgccgccc ccgccccgc gcagccagg cctgtccgcc 840
gcctacgaac gcccgtgca ccctatcgag agcgtatcg cgcgcgccgc catccatgcc 900
tccggcgctc accatcctgc gctccctgtg atcgccggcc gctccccgcg tctcgtcgcc 960
gacgcccacg acgtccacca gcgcagccc cccgcctacg cggccaccga ccccgccgcg 1020
gcctctccgc gcacccaacc gccccccatc cccgcaacaa acggctacgg cccggccgca 1080
cgagcccag ccacgctgac ccagccggcg ccgccaccgc cgcgcgccgc gcagcagcag 1140
cagcctccat cgacatcggc tcaaattccc cgcccaagc tcgccgaacc ctccaccacg 1200
gggaccacgg taccagcat cggggccctg atgaacggcg ccgcagccgg cggcggcctg 1260
ccctccatca cggccacggc agcgtcgacc ggccgcgccg acgggccccg cgatatcccc 1320
agcgagaaga tcgggttcgg cggcgaggat atgcgcgcgc tccgacaatt ggaccgcgtg 1380
ttcacggcg

```

<210> 80

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 80

```

Met Glu Thr Tyr Tyr Gly His Val Arg Thr Pro Ala Asp Ala Ile Ile
 1           5           10           15
Leu Phe Glu Ala Cys Arg Ile Gly Leu Leu Pro Arg Val Gln Arg Arg
 20           25           30
Leu Ser Glu Lys Glu Arg Gln Leu Ile Arg Ser Gly Ser Val Phe Val
 35           40           45
Trp Asp Glu Arg Glu Ala Gly Met Arg Arg Trp Thr Asp Gly Lys Ser
 50           55           60
Trp Ser Ala Ser Arg Val Ser Gly Ser Phe Leu Thr Tyr Arg Glu Met
 65           70           75           80
Glu Gly Lys Arg Gly Gly Thr Gly Val Ser Gln Ser Thr Ile Pro Arg
 85           90           95
Ala Gly Lys Thr Pro Glu Ser Thr Arg Gly Ser Asp Asp Asp Arg Gly
 100          105          110
Asp Gly Ala Asp Glu Gly Pro Asp Gly Tyr Arg Tyr Lys Pro Asp Gly
 115          120          125
Leu Met Lys Gln Ser Phe Ser Ile Thr Thr Ser Ala Gly Gln His Leu
 130          135          140
His Leu Ile Ser Tyr Tyr Ser Arg Ser His Pro Ser Ala Ala Asn Leu
 145          150          155          160
Gln Gln Pro Thr Asn Asp Pro Thr Leu Arg His Val Arg Pro Gln Lys
 165          170          175
Gly Leu Tyr Pro Glu Ser Thr Val Asn Asp Gln Gln Asn Leu Pro Val
 180          185          190
Val Thr Arg Gly Pro Met Gly Gly Ala Tyr Ser Val His His Pro Met
 195          200          205

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Pro Pro Tyr Ala Arg Ser Gly Ala Thr His Pro Gln Ser Tyr Thr Pro
 210      215      220
Pro Tyr Ala Trp Pro Pro Thr Pro Leu Ala Thr Pro Pro Val Thr Val
225      230      235      240
His Tyr Ser Pro Tyr Leu Pro Pro Val Ser Gly Ala Asn Gly Gln Leu
      245      250      255
Tyr Ala His His His Gln Pro Pro His Ala Gly Leu Pro Pro Pro Pro
      260      265      270
Pro Pro Gln Pro Gly Leu Ser Ala Ala Tyr Glu Arg Pro Val His Pro
      275      280      285
Ile Glu Ser Ala Ile Ala Pro Pro Ala Ile His Ala Ser Gly Val His
290      295      300
His Pro Ala Leu Pro Val Ile Ala Gly Arg Ser Pro Arg Leu Val Ala
305      310      315      320
Asp Ala His Asp Val His Gln Arg Ser Pro Pro Ala Tyr Ala Ala Thr
      325      330      335
Asp Pro Arg Arg Ala Ser Pro Arg Thr Gln Pro Pro Pro Ile Pro Ala
      340      345      350
Thr Asn Gly Tyr Gly Pro Ala Ala Arg Ser Pro Ala Thr Leu Thr Gln
      355      360      365
Pro Pro Pro Pro Pro Pro Pro Pro Pro Gln Gln Gln Gln Pro Pro Ser
      370      375      380
Thr Ser Ala Gln Ile Pro Pro Pro Lys Leu Ala Glu Pro Ser Thr Thr
385      390      395      400
Gly Thr Thr Val Pro Ser Ile Gly Ala Leu Met Asn Gly Ala Ala Ala
      405      410      415
Gly Gly Gly Leu Pro Ser Ile Thr Ala Thr Ala Ala Ser Thr Gly Arg
      420      425      430
Ala Asp Gly Pro Arg Asp Ile Pro Ser Glu Lys Ile Gly Phe Gly Gly
      435      440      445
Glu Asp Met Arg Ala Leu Arg Gln Leu Asp Arg Val Phe Thr Ala
      450      455      460

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<210> 81

<211> 2055

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 81

```

atgtcgtcgc ccaaggattc ccagtagcac acaacccttc ggcgccatcc ccgccggagg 60
gctgctttgt ccacttctcc tccatcttta cttattctt ccaactgtcg atctgtcgac 120
tcgaaccctt caaaccgctt gttcagaaag agcgaaacct ttcattgcag gagaaaccgt 180
cccacccac gcatcctcgt tctcagcttg cctcttgca cccgccgctc tctacatct 240
cccgctgccc tcgaagccat cgcggcgggc agagagcgca tgagcaagat cctcgatacc 300
ctcgacctcg ataccttcac tccctcgga tccgttgatg aggaactccc cgtgccccgc 360
agtgtcttgc aacttcattt cgactctttg catatctcgg accctcccca gactccgtcc 420
gtccgttcag ctcccaagaa gccgctccaa agagtcaacc atcacacttc cgacagcggt 480
ctcgggacct ctgtttgtag cgaagaagcg ctgtcttgta ccgaatccgc cgatctggac 540
tcgaacgccc ccatgtccgc ctcacatctt cggaaattgt cgctgacgg ggtcgacaag 600
atagagcacc gtgtcttcta cctcttctt atgaacacgc agttcgataa gttccacagc 660
actgttcgat atgccgctca aggggtcaag gacaatcgat tccgctgtct ccgtgacgtg 720
gaaaatttat tccgaatcc attccctatt gaccatgtta atgagaagga ggaattttct 780
cttttctga atcaggtggt cctgtgcttc gacgacactt ggcaccgcct cgatgaatcg 840

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gaccgcacta tgcctggtga tgtcccgtac tcgaatgagt acatcctcga cctttacgat 900
caaatcgctc gcttcaaggc gctctgtgag cgagcgaaac agactctctc gcagacggat 960
agcaacagtg ccaccccaaa gttgcccaag ctctgtttca aaggcggctt ggccaaaaca 1020
ggacgccagg cggaactggt cgctcagtcg gatgaccaga tgatgtcgct ccgcacgggt 1080
aaaccctacc aggagagcca ggtgccgagc atgaagcgtg gcctcagcct atgctcgacg 1140
gatggagagg gcgcccaccg atgcatggcc cgccgccgga agaacgaggc tcccatgaac 1200
atcaacactc cgtgcgactt ttgcgggcaa attttcgcga gaccctgtga cctcactaaa 1260
cacatgaaga cccacacacg cccgttcaag tgttcggtgc ctgagtgcaa gtactacacc 1320
tatggattcc cgactgaaaa ggagaaagac cgtcatttca acgacaagca caaccccgac 1380
ccggaaccgt acgaatgcga tctgggagga tgcaattatc gctctaagcg gttgagtaat 1440
ttgaagcagc ataaggagaa gaagcacggc tggcaatacg tccggaccaaa gagcaacggc 1500
aagcgcaagg agaagggcaa gggcaagaaa gccagtcctc agtctactcc ggatactccc 1560
ggccttacca ctcccgccac cagcacccgg cagtccttct cgactccgaa cactggaccc 1620
agtccgtccc ccccgagggc agtctcccga cctctgccga ctaccgactt caactttgct 1680
gatcctccgt tgcccacccc ggttgccggac ttccaactgt tcaacgcgaa cagccccatg 1740
ggagggaaac gaagcgtgaa catgggttat gcggatttgg gctttccgga aatgactcgg 1800
tcaatggacg gcgacgtggt tcatatgaac aactttgaag acatgttcgc caacgtcaac 1860
aacccttacc tggaatggact cagcgggggt tatcaagtcc ccagcggcta tgaagccggc 1920
aacattgact ttccgatctt gggttatggc acggccgtgc ctccgtctgc ggtcttccac 1980
gaagaccaat tcctgccgga gacgatcaac tgggaagaat tcgccatgct taacggaatg 2040
gatacgatgt ccaag                                     2055

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<210> 82

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 82

```

Met Ser Ser Pro Lys Asp Ser Gln Tyr Asp Thr Thr Leu Arg Arg His
 1          5          10          15
Pro Arg Arg Arg Ala Ala Leu Ser Thr Ser Pro Pro Ser Leu Leu Asn
      20          25          30
Ser Ser Asn Cys Arg Ser Val Asp Ser Asn Pro Ser Asn Pro Leu Phe
      35          40          45
Arg Lys Ser Glu Thr Phe His Ala Ala Arg Asn Arg Pro Thr Pro Arg
      50          55          60
Asp Pro Arg Leu Ser Leu Pro Leu Ala Pro Arg Arg Ser Pro Thr Ser
      65          70          75          80
Pro Ala Ala Leu Glu Ala Ile Ala Ala Gly Arg Glu Arg Met Ser Lys
      85          90          95
Ile Leu Asp Thr Leu Asp Leu Asp Thr Phe Thr Pro Ser Glu Ser Val
      100          105          110
Asp Glu Glu Leu Pro Val Pro Arg Ser Val Leu Gln Leu His Phe Asp
      115          120          125
Ser Leu His Ile Ser Asp Pro Pro Gln Ser Pro Ser Val Arg Ser Ala
      130          135          140
Pro Lys Lys Pro Leu Gln Arg Val Asn His His Thr Ser Asp Ser Gly
      145          150          155          160
Leu Gly Thr Ser Val Cys Ser Glu Glu Ala Leu Ser Cys Thr Glu Ser
      165          170          175
Ala Asp Leu Asp Ser Asn Ala Pro Met Ser Ala Ser His Leu Arg Lys
      180          185          190
Leu Ser Pro Asp Gly Val Asp Lys Ile Glu His Arg Val Phe Tyr Pro
      195          200          205

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Leu Leu Met Asn Thr Gln Phe Asp Lys Phe His Ser Thr Val Arg Tyr
210                215                220
Ala Ala Gln Gly Val Lys Asp Asn Arg Phe Arg Cys Leu Arg Asp Val
225                230                235                240
Glu Asn Leu Phe Arg Asn Pro Phe Pro Ile Asp His Val Asn Glu Lys
                245                250                255
Glu Glu Phe Ser Leu Phe Leu Asn Gln Val Val Leu Cys Leu Asp Asp
                260                265                270
Thr Trp His Arg Leu Asp Glu Ser Asp Arg Thr Met Pro Gly Asp Val
                275                280                285
Pro Tyr Ser Asn Glu Tyr Ile Leu Asp Leu Tyr Asp Gln Ile Val Arg
290                295                300
Phe Lys Ala Leu Cys Glu Arg Ala Lys Gln Thr Leu Ser Gln Thr Asp
305                310                315                320
Ser Asn Ser Ala Thr Pro Lys Leu Pro Lys Leu Val Phe Lys Gly Gly
                325                330                335
Leu Ala Lys Thr Gly Arg Gln Ala Glu Leu Val Ala Gln Ser Asp Asp
                340                345                350
Gln Met Met Ser Leu Arg Thr Gly Lys Pro Tyr Gln Glu Ser Gln Val
                355                360                365
Pro Ser Met Lys Arg Gly Leu Ser Leu Cys Ser Thr Asp Gly Glu Gly
370                375                380
Ala His Arg Cys Met Ala Arg Arg Arg Lys Asn Glu Ala Pro Met Asn
385                390                395                400
Ile Asn Thr Pro Cys Asp Phe Cys Gly Gln Ile Phe Ala Arg Pro Cys
                405                410                415
Asp Leu Thr Lys His Met Lys Thr His Thr Arg Pro Phe Lys Cys Ser
                420                425                430
Val Pro Glu Cys Lys Tyr Tyr Thr Tyr Gly Phe Pro Thr Glu Lys Glu
                435                440                445
Lys Asp Arg His Phe Asn Asp Lys His Asn Pro Asp Pro Glu Pro Tyr
450                455                460
Glu Cys Asp Leu Gly Gly Cys Asn Tyr Arg Ser Lys Arg Leu Ser Asn
465                470                475                480
Leu Lys Gln His Lys Glu Lys Lys His Gly Trp Gln Tyr Val Arg Thr
                485                490                495
Lys Ser Asn Gly Lys Arg Lys Glu Lys Gly Lys Lys Lys Ala Ser
                500                505                510
Pro Gln Ser Thr Pro Asp Thr Pro Gly Leu Thr Thr Pro Gly Thr Ser
                515                520                525
Thr Ala Gln Ser Phe Ser Thr Pro Asn Thr Gly Pro Ser Pro Ser Pro
530                535                540
Pro Gln Ala Val Ser Arg Pro Leu Pro Thr Thr Asp Phe Asn Phe Ala
545                550                555                560
Asp Pro Pro Leu Pro Thr Pro Val Ala Asp Phe Gln Leu Phe Asn Ala
                565                570                575
Asn Ser Pro Met Gly Gly Asn Gly Ser Val Asn Met Gly Tyr Ala Asp
                580                585                590
Leu Gly Phe Pro Glu Met Thr Arg Ser Met Asp Gly Asp Val Val His
                595                600                605
Met Asn Asn Phe Glu Asp Met Phe Ala Asn Val Asn Asn Pro Tyr Leu
610                615                620
Asp Gly Leu Ser Gly Gly Tyr Gln Val Pro Ser Gly Tyr Glu Ala Gly
625                630                635                640
Asn Ile Asp Phe Pro Asp Leu Gly Tyr Gly Thr Ala Val Pro Pro Ser
                645                650                655
Ala Val Phe His Glu Asp Gln Phe Leu Pro Glu Thr Ile Asn Trp Glu

```

660  
 Glu Phe Ala Met Leu Asn Gly Met Asp Thr Met Ser Lys  
 675 680 685

<210> 83  
 <211> 1239  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 83  
 atggtcaaca cccacccga tcaacggccc cagctctccc cgtccaaccc caatcccccg 60  
 tctcgacgac gcaatgatcg cgacatctac gtcgccgatg ccagtgaagg cgccaccccg 120  
 cgccccatgg acgataccca ccccgccgcc gccacgcgcg ccgttgccct ggcccaatta 180  
 caccacaatc gcttggtctc cgactgggag acggacatgg aatcccactc cgacaatgac 240  
 atcagccgcg accgcatgcg atcctccatc gagctcccct ctctgcgcga ccacttcaag 300  
 caggactccc tcccaccctt ctcccgcgga ccgcgcgaac tgctcccctc catcctcaac 360  
 cactcgcccc caggctcgctc ctccactctt ccccccatcc agcaaaagaa gtggccgcgc 420  
 ccgcgcaaat cctccatctc cggcgctcgc aagcccaaac atgaacgctc caagtccaag 480  
 gagtacggtc gccgccccag cttaggcgat cgcaaagccc tgtccgccga accccagacc 540  
 gccgcctggg ctacgggcaa gcgctgggag gatctgatcg aagccgcgac ttcggcgacc 600  
 gaggccgacg acgaacgccca ttctgagggtc ggtcggctgc ccaccatccc tccggtgtcc 660  
 agcttcacct ccgcccccat ggggaagaat cgctcgctgc ttcccccggg attccaagga 720  
 ctaccacccc ccacctcgca tcgtccgttc ccgctcctc cctacgcgcg gtcgccgttg 780  
 aacaacgacc tggagccctt cccctcgata gattcgctcc tcgactccgc ctgcaccgcg 840  
 tccggaaga cctccacta taatcacgtc ggtccggcca acgactccag tccggtgctg 900  
 aacatgttcc cgtcgtcggc cgtgcagcgc caacaccatc gcttttccaa cccaccccc 960  
 gcctccatgc ggagccgcga gatccagatc tattgcgcc actgcaagcg accgtgggcg 1020  
 ctcaacgaat gctacgcctg caccgagtg atctgcggcg tctgtcgcga atgtgtcgga 1080  
 atgttcacg gcagcccgcc cactccttc cgcaacgtca cctccagccc gggcagtgcc 1140  
 ttgccccacg gcccgaccag ctatcctagc gcccgaggtt gtccccgctg tcgcaccgtc 1200  
 ggcggcaagt ggaaggcttt tcagctggat ttcaagtag 1239

<210> 84  
 <211> 412  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 84  
 Met Val Asn Thr Pro Pro Asp Gln Arg Pro Gln Leu Ser Pro Ser Asn  
 1 5 10 15  
 Pro Asn Pro Pro Ser Arg Arg Arg Asn Asp Arg Asp Ile Tyr Val Ala  
 20 25 30  
 Asp Ala Ser Glu Pro Ala Thr Pro Arg Pro Met Asp Asp Thr His Pro  
 35 40 45  
 Ala Ala Ala Thr Ala Ala Val Ala Leu Ala Gln Leu His His Asn Arg  
 50 55 60  
 Leu Val Ser Asp Trp Glu Thr Asp Met Glu Ser His Ser Asp Asn Asp  
 65 70 75 80  
 Ile Ser Arg Asp Arg Met Arg Ser Ser Ile Glu Leu Pro Ser Leu Arg  
 85 90 95

```

Asp His Phe Lys Gln Asp Ser Leu Pro Pro Phe Ser Pro Arg Pro Arg
      100      105      110
Glu Leu Leu Pro Ser Ile Leu Asn His Ser Pro Pro Gly Arg Ser Ser
      115      120      125
Thr Leu Pro Pro Ile Gln Gln Lys Lys Trp Pro Arg Pro Arg Lys Ser
      130      135      140
Ser Ile Ser Gly Ala Arg Lys Pro Lys His Glu Arg Ser Lys Ser Lys
      145      150      155      160
Glu Tyr Gly Arg Arg Pro Ser Leu Gly Asp Arg Lys Ala Leu Ser Ala
      165      170      175
Glu Pro Gln Thr Ala Ala Trp Ala Gln Gly Lys Arg Trp Glu Asp Leu
      180      185      190
Ile Glu Ala Ala Thr Ser Ala Thr Glu Ala Asp Asp Glu Arg His Ser
      195      200      205
Glu Val Gly Arg Ser Pro Thr Ile Pro Pro Val Ser Ser Phe Thr Ser
      210      215      220
Ala Pro Met Gly Lys Asn Arg Ser Ser Leu Pro Pro Gly Phe Gln Gly
      225      230      235      240
Leu Pro Pro Pro Thr Ser His Arg Pro Phe Pro Pro His Pro Tyr Ala
      245      250      255
Ala Ser Pro Leu Asn Asn Asp Leu Glu Pro Phe Pro Ser Ile Glu Ser
      260      265      270
Ser Leu Asp Ser Ala Ser Thr Ala Ser Gly Lys Thr Leu His Tyr Asn
      275      280      285
His Val Gly Pro Ala Asn Asp Ser Ser Pro Val Leu Asn Met Phe Pro
      290      295      300
Ser Ser Ala Val Gln Arg Gln His His Arg Phe Ser Asn Pro Thr Pro
      305      310      315      320
Ala Ser Met Arg Ser Arg Glu Ile Gln Ile Tyr Cys Ala His Cys Lys
      325      330      335
Arg Pro Trp Ala Leu Asn Glu Cys Tyr Ala Cys Thr Glu Cys Ile Cys
      340      345      350
Gly Val Cys Arg Glu Cys Val Gly Met Phe Ile Gly Ser Pro Pro Thr
      355      360      365
Ser Phe Arg Asn Val Thr Ser Ser Pro Gly Ser Ala Leu Pro His Gly
      370      375      380
Pro Thr Ser Tyr Pro Ser Ala Arg Gly Cys Pro Arg Cys Arg Thr Val
      385      390      395      400
Gly Gly Lys Trp Lys Ala Phe Gln Leu Asp Phe Lys
      405      410

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&lt;210&gt; 85

&lt;211&gt; 282

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 85

```

atgctggaca ttccgaagga catcgagaag atctcgatcc ctgtgagctt tgccttgggc 60
gagcatgaca ggcgaatcaa gccggctcag gtcactcaga tcaagcaaac tctgaatgca 120
aaggaagaga atgtggctag tgaagtgaag atgtattacg gtgttggtca cggcttctgc 180
gtgagagcgg ataccaaact ggtggacgca gacacacaag caactgaggc agagaatcag 240
gccctggctt gggtcaatcg tcatttcgcg gacttttcat cc 282

```

<210> 86  
 <211> 94  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 86  
 Met Leu Asp Ile Pro Lys Asp Ile Glu Lys Ile Ser Ile Pro Val Ser  
 1 5 10 15  
 Phe Ala Leu Gly Glu His Asp Ser Ala Ile Lys Pro Ala Gln Val Thr  
 20 25 30  
 Gln Ile Lys Gln Thr Leu Asn Ala Lys Glu Glu Asn Val Ala Ser Glu  
 35 40 45  
 Val Lys Met Tyr Tyr Gly Val Gly His Gly Phe Cys Val Arg Ala Asp  
 50 55 60  
 Thr Lys Leu Val Asp Ala Asp Thr Gln Ala Thr Glu Ala Glu Asn Gln  
 65 70 75 80  
 Ala Leu Ala Trp Phe Asn Arg His Phe Ala Asp Phe Ser Ser  
 85 90

<210> 87  
 <211> 378  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 87  
 atgtctagcc aacctctcct ccaaaccgct cggggcaage gaattgccct cccaaccgca 60  
 gtcgaaccca aggtcttctt cgctaacgag cgcaccttcc tctcatggct taacttcacc 120  
 gtcattcctgg gcggcctagc ggtcggcctc ctcaatttgc gcgaccgcat cggtcgcata 180  
 tccgcagctc tcttcaccat catcgcatg ggcgcaatga tctacgcctt ggtgacattc 240  
 cactggcgcg cgcagagtat ccgtcggcgc ggacagagcg gtatcgatga ccgattcggg 300  
 cctaccatcc tggccattgc cctcctcgcc gccgtcggtg ttaacttcatt cttgcggatt 360  
 aaggacgggc agatgaac 378

<210> 88  
 <211> 126  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 88  
 Met Ser Ser Gln Pro Leu Leu Gln Thr Ala Pro Gly Lys Arg Ile Ala  
 1 5 10 15  
 Leu Pro Thr Arg Val Glu Pro Lys Val Phe Phe Ala Asn Glu Arg Thr  
 20 25 30  
 Phe Leu Ser Trp Leu Asn Phe Thr Val Ile Leu Gly Gly Leu Ala Val  
 35 40 45  
 Gly Leu Leu Asn Phe Gly Asp Arg Ile Gly Arg Ile Ser Ala Ala Leu  
 50 55 60

```

Phe Thr Ile Ile Ala Met Gly Ala Met Ile Tyr Ala Leu Val Thr Phe
65          70          75          80
His Trp Arg Ala Gln Ser Ile Arg Arg Arg Gly Gln Ser Gly Ile Asp
          85          90          95
Asp Arg Phe Gly Pro Thr Ile Leu Ala Ile Ala Leu Leu Ala Ala Val
          100        105        110
Val Val Asn Phe Ile Leu Arg Ile Lys Asp Gly Gln Met Asn
          115        120        125

```

<210> 89  
 <211> 387  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

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<400> 89
atgcatgatg actctggaaa aagcggcctg caaatccaaa acgtcgagac gggggggttg 60
ctagaggtca cgaactccgg gacgcgagtc cagtgtggga tgacggaagt cggtagcgag 120
acggtctggg atcttgtctt gcttcctacg ccatacgtccc tgcttcaagg gttggcgggc 180
acaggggdcgg cttctcgtgg tggctctagc cgctcgtcgc gccctcgtgg gcgacgggat 240
gacgatgagg atacgaggaa agactctgac tcctctgtat tggaatatag tgatgactct 300
tgtgacgatg ggtggacgat tagggcagac cccgttgtga ggcacgcaga cggcctggcg 360
catcaggaca ttaccatgcg caaatgc                                     387

```

<210> 90  
 <211> 129  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

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<400> 90
Met His Asp Asp Ser Gly Lys Ser Gly Leu Gln Ile Gln Asn Val Glu
1          5          10          15
Thr Gly Gly Trp Leu Glu Val Thr Asn Ser Gly Thr Arg Val Gln Cys
          20          25          30
Gly Met Thr Glu Val Gly Ser Glu Thr Val Trp Asp Leu Val Leu Leu
          35          40          45
Pro Thr Pro Ser Ser Leu Leu Gln Gly Leu Ala Gly Thr Gly Ala Ala
          50          55          60
Ser Arg Gly Gly Ser Ser Arg Ser Ser Arg Pro Arg Gly Arg Arg Asp
65          70          75          80
Asp Asp Glu Asp Thr Arg Lys Asp Ser Asp Ser Ser Val Leu Glu Tyr
          85          90          95
Ser Asp Asp Ser Cys Asp Asp Gly Trp Thr Ile Arg Ala Asp Pro Val
          100        105        110
Val Arg His Arg Asp Gly Leu Ala His Gln Asp Ile Thr Met Arg Lys
          115        120        125
Cys

```

<210> 91

&lt;211&gt; 2274

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 91

```

atgatctccg ctccgggtcc cgagcgacgg cgagacggc cggcagtgct atgtttctctt 60
tgcagaaggc gtaagattaa atgcaaccgc gaaagcccct gtagcaactg catcaagtct 120
aaggcggaac catgctgcta cgagagcgac tcctcgcccc ggccgcagca gcatcttggc 180
ttcaatcaga cactggagct agggctctgc aaggcgctctg aagccagat gctccctcca 240
gatgcggtaa cttctcaagt tcttagctat gcgtccaggc cattactctc cagcgcgaga 300
gactcgatcat cccggacgag tcaagcttct gcacggagg ttgagtctct gaagaccaag 360
atcagacagc tggaggaaaca gctgtccagt gcgacgcagc cggcggaatc acctccacgg 420
ccgtctccaa actccagaat cgagaccagc acgtctcaga tagcagggac gttccacata 480
aaccatgaaa ggcggttct ccacgattcc cagttcgtca accgaaatct ggtcatacat 540
aaaagtcgac tgtttggctc cagtcattgg gcacaggctg catcgatgtt tagagatgta 600
tttgaaatga tcgaaccgtt tatccgcggg agtgggtcca aagccagtgc cggcatcaga 660
aggtgcaaag agctggcaag gattatcaaa acccaacgga cgccgcaatg gccgacgccg 720
cccactcagg atctacctcc aaaaggcgct gctgatgagt tggttgactg ctatctccgt 780
acaatcgaga ctacattccg ggtcctgcac gtacctacat tcaggtccga atatgacgct 840
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gcactggggt ctgtcactta cgacgagcgg ttttcaatga gaccagtgct ggttcgttgg 960
gtatttgagg cgcacacctg gctctctgat ccagacttca aacctcaact taacatacag 1020
tgtttgcaaa gcaggattct actattacta gcccgcgaga taatcaatgt tgggtggcgat 1080
tcgagttgga tatctgccgg cggactactc cgcactgctc tacatatggg attacatagg 1140
gatccgtctg tactgccgcc taggtcggcg ctcgctgttg aaatgcgacg ccgactgtgg 1200
aacactatcc tcgagctatc actgcagtca agcatttccct ccggtggacc tccactaatt 1260
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aggggaacct acccacagcg ccttgcaatt gtgaaattcc tgaacgatct aagttcatat 1440
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ggtgttataa tcgcggccat gttcgtgacc ttggagctta aagctcagct cctggatgat 1860
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gaccgttggt ggaatatgat tcaatgtggt gagactaatg tcaagggcta cctcctcatt 1980
tgtctggtaa ccgcccagat cgaggggctg atgcatggag ttgaaccgag caaactcccc 2040
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aaagccgacg tgggacggag tgggtggttc gttgaggtga tggacgaatc tgcgaataca 2160
gcgcccttca tgggcgactg ggagtttatt atgacagatc ctttccttaa ttatcctggg 2220
actactgaac cactcagctg ggttatgaat gaagaaacga gaccattcat aatg 2274

```

&lt;210&gt; 92

&lt;211&gt; 758

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 92

Met Ile Ser Ala Pro Gly Pro Glu Arg Arg Arg Arg Pro Ala Val

1				5					10				15				
Ser	Cys	Ser	Leu	Cys	Arg	Arg	Arg	Lys	Ile	Lys	Cys	Asn	Arg	Glu	Ser		
			20					25				30					
Pro	Cys	Ser	Asn	Cys	Ile	Lys	Ser	Lys	Ala	Glu	Pro	Cys	Val	Tyr	Glu		
	35						40					45					
Ser	Asp	Ser	Ser	Ser	Arg	Pro	Gln	Gln	His	Leu	Gly	Phe	Asn	Gln	Thr		
	50					55					60						
Leu	Glu	Leu	Gly	Leu	Cys	Lys	Ala	Ser	Glu	Arg	Gln	Met	Leu	Pro	Pro		
65					70					75				80			
Asp	Ala	Val	Thr	Ser	Gln	Val	Pro	Ser	Tyr	Ala	Ser	Arg	Ser	Leu	Leu		
				85					90					95			
Ser	Ser	Ala	Arg	Asp	Ser	Ser	Ser	Arg	Thr	Ser	Gln	Ala	Ser	Ala	Ser		
			100					105					110				
Glu	Val	Glu	Ser	Leu	Lys	Thr	Lys	Ile	Arg	Gln	Leu	Glu	Glu	Gln	Leu		
		115					120					125					
Ser	Ser	Ala	Thr	Gln	Pro	Ala	Glu	Ser	Pro	Pro	Arg	Pro	Ser	Pro	Asn		
	130					135					140						
Ser	Arg	Ile	Glu	Thr	Ser	Thr	Ser	Gln	Ile	Ala	Gly	Thr	Phe	His	Ile		
145					150					155					160		
Asn	His	Glu	Arg	Arg	Leu	Leu	His	Asp	Ser	Gln	Phe	Val	Asn	Arg	Asn		
				165				170					175				
Leu	Val	Ile	His	Lys	Ser	Arg	Leu	Phe	Gly	Ser	Ser	His	Trp	Ala	Gln		
			180					185					190				
Ala	Ala	Ser	Met	Phe	Arg	Asp	Val	Phe	Glu	Met	Ile	Glu	Pro	Phe	Ile		
		195					200					205					
Arg	Gly	Ser	Gly	Ser	Lys	Ala	Ser	Ala	Gly	Ile	Arg	Arg	Cys	Lys	Glu		
	210					215					220						
Leu	Ala	Arg	Ile	Ile	Lys	Thr	Gln	Arg	Thr	Pro	Gln	Trp	Pro	Thr	Pro		
225					230					235				240			
Pro	Thr	Gln	Asp	Leu	Pro	Pro	Lys	Gly	Val	Ala	Asp	Glu	Leu	Val	Asp		
				245					250					255			
Cys	Tyr	Leu	Arg	Thr	Ile	Glu	Thr	Thr	Phe	Arg	Val	Leu	His	Val	Pro		
			260					265					270				
Thr	Phe	Arg	Ser	Glu	Tyr	Asp	Ala	Leu	Trp	Val	Ser	Glu	Ala	Arg	Pro		
		275					280					285					
Ser	Ile	Ala	Phe	Thr	Val	Gln	Leu	Lys	Leu	Val	Leu	Ala	Leu	Gly	Ser		
	290					295					300						
Val	Thr	Tyr	Asp	Glu	Arg	Phe	Ser	Met	Arg	Pro	Ser	Ala	Val	Arg	Trp		
305					310					315				320			
Val	Phe	Glu	Ala	His	Thr	Trp	Leu	Ser	Asp	Pro	Asp	Phe	Lys	Pro	Gln		
				325					330					335			
Leu	Asn	Ile	Gln	Cys	Leu	Gln	Ser	Arg	Ile	Leu	Leu	Leu	Leu	Ala	Arg		
			340					345					350				
Glu	Ile	Ile	Asn	Val	Gly	Gly	Asp	Ser	Ser	Trp	Ile	Ser	Ala	Gly	Gly		
		355					360					365					
Leu	Leu	Arg	Thr	Ala	Leu	His	Met	Gly	Leu	His	Arg	Asp	Pro	Ser	Val		
	370					375					380						
Leu	Pro	Pro	Arg	Ser	Ala	Leu	Ala	Val	Glu	Met	Arg	Arg	Arg	Leu	Trp		
385					390					395				400			
Asn	Thr	Ile	Leu	Glu	Leu	Ser	Leu	Gln	Ser	Ile	Ser	Ser	Gly	Gly			
				405					410				415				
Pro	Pro	Leu	Ile	Ser	Leu	Gly	Asp	Phe	Asp	Cys	Ala	Pro	Pro	Gly	Asn		
			420					425					430				
Phe	Asp	Asp	Glu	Gln	Leu	Leu	Ala	Glu	Asp	Pro	Val	Pro	Lys	Ser	Asp		
		435					440					445					
Asp	Glu	Tyr	Thr	Gln	Thr	Ala	Ile	Ala	Arg	Ala	Leu	Arg	Gly	Thr	Tyr		
	450					455					460						



Pro Gln Arg Leu Ala Ile Val Lys Phe Leu Asn Asp Leu Ser Ser Tyr  
 465 470 475 480  
 Gly Thr Tyr Glu Glu Thr Leu Arg Leu Asp Ala Asp Leu Arg Glu Ser  
 485 490 495  
 Tyr Arg Ala Ile Cys Arg Ile Leu Arg Gly Tyr Pro Ser Asn Gly Pro  
 500 505 510  
 Ser Pro Ser Gln Phe Glu Lys Cys Met Leu Asp Phe Ile Ile His Phe  
 515 520 525  
 Tyr Val Cys Cys Leu His Ile Pro Tyr Ile Glu Lys Ser Leu Arg Ala  
 530 535 540  
 Pro Ala Tyr Ala Phe Ser Arg Lys Val Ala Ile Glu Ser Ala Leu Lys  
 545 550 555 560  
 Met Trp Cys Ala Ile Tyr Pro Ser Ser Arg Phe Met Ser Asn Thr Arg  
 565 570 575  
 Arg Glu Ile Ser Gly Ser Val Glu Asn Lys Leu Thr Arg Phe Val Glu  
 580 585 590  
 Cys Gly Phe Gly Phe Phe Arg Thr Gly Val Ile Ile Ala Ala Met Phe  
 595 600 605  
 Val Thr Leu Glu Leu Lys Ala Gln Leu Leu Asp Asp Ser Leu Gly  
 610 615 620  
 Pro Ser Pro Tyr Arg Val Asp Leu Phe Ser Leu Leu Cys Glu Ala Lys  
 625 630 635 640  
 Asp Arg Cys Trp Asn Met Ile Gln Cys Gly Glu Thr Asn Val Lys Gly  
 645 650 655  
 Tyr Leu Leu Ile Cys Leu Val Thr Ala Gln Ile Glu Gly Leu Met His  
 660 665 670  
 Gly Val Glu Pro Ser Lys Leu Pro Glu Leu Leu Leu Arg Ala Ala Glu  
 675 680 685  
 Glu Ala Glu Asp Arg Cys Leu Asp Phe Met Glu Glu Lys Ala Asp Leu  
 690 695 700  
 Gly Arg Ser Gly Gly Ser Val Glu Val Met Asp Glu Ser Ala Asn Thr  
 705 710 715 720  
 Ala Pro Phe Met Gly Asp Trp Glu Phe Ile Met Thr Asp Pro Phe Leu  
 725 730 735  
 Asn Tyr Pro Gly Thr Thr Glu Pro Leu Ser Trp Val Met Asn Glu Glu  
 740 745 750  
 Thr Arg Pro Phe Ile Met  
 755

&lt;210&gt; 93

&lt;211&gt; 1530

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 93

atgaccagca caatagcccg cactgaggaa cgccagaacg ctggcaccat tgaactgaaa 60  
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 cctgcaactgt tcggtcttta ccgtaacaaa ttctcctcca aggggatcaa gatcgtcgga 180  
 tatgctcgga cgaacatgga ccacgaagaa tatctgagac ggggtgcgctc gtacatcaag 240  
 acccccacca aggaaatcga agaacagctg gatggcttct gccagctgtg cacctacatc 300  
 agcggccaat atgacaagga tgactcgttc attaacctca ctaagcacct cgaggacgtc 360  
 gagaagggcc ataaggaaca gaacagagtc ttctacatgg cgctgcctcc tagcgtcttc 420  
 attaccgtgt cggatcaatt gaagagaaac tgctacccca agaacggcat tgcccgtatt 480

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attgtcgaga agcccttcgg caaggatctc cagagttctc gtgacctcca gaaggccctt 540
gagcccaact ggaaagagga ggagatcttc cgtattgacc actacctggg taaggagatg 600
gtcaagaaca tcctcatcat gcgcttcgga aacgagttct tcaacgctac ctggaaccgt 660
caccacattg ataacgtgca gatcacattc aaggagccgt tcggcacgga gggccgtgga 720
ggctactttg atgagttcgg catcattcgt gatgtcatgc agaaccacct tctgcagggtg 780
ttgacgcttc ttgccatgga gcgtcccatc tctttctctg ctgaagacat tctgtacgag 840
aaggtgcgtg ttctgcgcgc gatggacccc attgagccca agaacgtcat catcggccag 900
tacggaaagt cgctcgacgg tagcaagccc gcctacaagg aggatgatac tgtgcctcaa 960
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ggcgttccct tcatcatgaa ggccggtaaa gccctgaacg agcagaagac cgagatccgt 1080
atccagttcc gtgacgtcac ttccggcatc ttcaaggaca tccccgcaa cgaacttgct 1140
attcgtgtcc agcccaacga gtccgtgtac attaatga actcgaagct accgggtctc 1200
tccatgcaga cggctgttac cgagcttgac cttacctacc gccgcgcttt ctccgacctc 1260
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tttgtcogtg acgatgaact tgactcgagc tggaagatct tcacctctct gctgcactac 1380
ctggacgaca acaaggagat tatcccatg gaataccct acggctctcg cggacctgct 1440
gtgctcgacg acttcaccgc gtccgttcggg tacaagttca gtgatgctgc tggctaccag 1500
tggccctga ctccggtcc caacagactg 1530

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<210> 94

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 94

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Met Thr Ser Thr Ile Ala Arg Thr Glu Glu Arg Gln Asn Ala Gly Thr
 1          5          10          15
Ile Glu Leu Lys Asp Asp Thr Val Ile Val Val Leu Gly Ala Ser Gly
          20          25          30
Asp Leu Ala Lys Lys Lys Thr Phe Pro Ala Leu Phe Gly Leu Tyr Arg
          35          40          45
Asn Lys Phe Leu Pro Lys Gly Ile Lys Ile Val Gly Tyr Ala Arg Thr
          50          55          60
Asn Met Asp His Glu Glu Tyr Leu Arg Arg Val Arg Ser Tyr Ile Lys
65          70          75          80
Thr Pro Thr Lys Glu Ile Glu Glu Gln Leu Asp Gly Phe Cys Gln Leu
          85          90          95
Cys Thr Tyr Ile Ser Gly Gln Tyr Asp Lys Asp Asp Ser Phe Ile Asn
          100          105          110
Leu Thr Lys His Leu Glu Asp Val Glu Lys Gly His Lys Glu Gln Asn
          115          120          125
Arg Val Phe Tyr Met Ala Leu Pro Pro Ser Val Phe Ile Thr Val Ser
          130          135          140
Asp Gln Leu Lys Arg Asn Cys Tyr Pro Lys Asn Gly Ile Ala Arg Ile
145          150          155          160
Ile Val Glu Lys Pro Phe Gly Lys Asp Leu Gln Ser Ser Arg Asp Leu
          165          170          175
Gln Lys Ala Leu Glu Pro Asn Trp Lys Glu Glu Glu Ile Phe Arg Ile
          180          185          190
Asp His Tyr Leu Gly Lys Glu Met Val Lys Asn Ile Leu Ile Met Arg
          195          200          205
Phe Gly Asn Glu Phe Phe Asn Ala Thr Trp Asn Arg His His Ile Asp
          210          215          220
Asn Val Gln Ile Thr Phe Lys Glu Pro Phe Gly Thr Glu Gly Arg Gly

```

225		230		235		240
Gly Tyr Phe Asp	Glu Phe Gly Ile Ile Arg Asp Val Met Gln Asn His					
	245		250		255	
Leu Leu Gln Val	Leu Thr Leu Leu Ala Met Glu Arg Pro Ile Ser Phe					
	260		265		270	
Ser Ala Glu Asp	Ile Arg Asp Glu Lys Val Arg Val Leu Arg Ala Met					
	275		280		285	
Asp Pro Ile Glu	Pro Lys Asn Val Ile Ile Gly Gln Tyr Gly Lys Ser					
	290		295		300	
Leu Asp Gly Ser	Lys Pro Ala Tyr Lys Glu Asp Asp Thr Val Pro Gln					
305		310		315		320
Asp Ser Arg Cys	Pro Thr Phe Cys Ala Met Val Ala Tyr Ile Lys Asn					
	325		330		335	
Glu Arg Trp Asp	Gly Val Pro Phe Ile Met Lys Ala Gly Lys Ala Leu					
	340		345		350	
Asn Glu Gln Lys	Thr Glu Ile Arg Ile Gln Phe Arg Asp Val Thr Ser					
	355		360		365	
Gly Ile Phe Lys	Asp Ile Pro Arg Asn Glu Leu Val Ile Arg Val Gln					
	370		375		380	
Pro Asn Glu Ser	Val Tyr Ile Lys Met Asn Ser Lys Leu Pro Gly Leu					
385		390		395		400
Ser Met Gln Thr	Val Val Thr Glu Leu Asp Leu Thr Tyr Arg Arg Arg					
	405		410		415	
Phe Ser Asp Leu	Lys Ile Pro Glu Ala Tyr Glu Ser Leu Ile Leu Asp					
	420		425		430	
Ala Leu Lys Gly	Asp His Ser Asn Phe Val Arg Asp Asp Glu Leu Asp					
	435		440		445	
Ser Ser Trp Lys	Ile Phe Thr Pro Leu Leu His Tyr Leu Asp Asp Asn					
	450		455		460	
Lys Glu Ile Ile	Pro Met Glu Tyr Pro Tyr Gly Ser Arg Gly Pro Ala					
465		470		475		480
Val Leu Asp Asp	Phe Thr Ala Ser Phe Gly Tyr Lys Phe Ser Asp Ala					
	485		490		495	
Ala Gly Tyr Gln	Trp Pro Leu Thr Ser Ala Pro Asn Arg Leu					
	500		505		510	

<210> 95  
 <211> 2550  
 <212> DNA  
 <213> Artificial Sequence.

<220>  
 <223> fungal gene

<400> 95  
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 cattatcgag tcatccgaaa gcgaaaccgg gtgcctctat cctgcggccc ctgccgacat 120  
 agaaaaactca aatgcaaccg tgctcatcca tgtgaaaact gcgtcaaacg gggcgatgcc 180  
 tcgtcctgta cctatgcaca agccaacgcg cggaaaaaga actcaccgct tcagaccgct 240  
 tcgagctcac ccgacgacat gcaaaaccgg atagatcgct ttgagagctt ggtgctctct 300  
 ttgatgacca atggatctca gtccgcaggc cccacggcag ctatggcggg catttccggc 360  
 aactccagca gcatcggctc cgctcaacat acgtcgggaag atgtagagct ggacgatgat 420  
 gatgggcaag gtcccagga gagtgatacg gagcaattga ccaagtcgat cggatatcatg 480  
 aaggtcgaca acaacaaatc gtggtatatc agtgatgcac attgggcatc ggtcctgagc 540  
 gatatagcgg aagtcaaaaa ttacttcaac acgcacaaga agcaatatga agaacacgca 600  
 gagaaaatta aagcgacgcg actcccaaca gatgttcccg gctcgacctt gctcttcggt 660

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gggacgaaaa cgataagtcg cgaggaaatc atggcctctt tcccatccag gtatactgcg 720
gatatcctcg ttgcgcgcta tttcaaccac tatgaccctt ccacgcacat tcttcattggc 780
cctacctttc aggcgcagta caataaacac tgggaggacc cctccaaaac ctgtattgtt 840
tggatcggtg tgctttttgc tatgatgcga ctgcctatgc tctcatatca tcgcgagggc 900
gacgaacctc cggagtttcg cgggaaggcg ctggacatgg cgggcacata ccggaatctc 960
atggcccagt gtttgacgtt ggcgactac accaaaccgt acccttgttt gatcgaatct 1020
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cggcaagcag acttgctctt ttctgccccaa gtgcgcctgc ccagcatgat tcgcacttcg 1260
gatagtgata cggagctacc acgcaatctc tatgacgacg attttgacga gaattgcacg 1320
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gcccgtatca catatgcttt cggccgcggt atagaagaca catcttctct ccgaagcgct 1440
ccatacgaca aggtcatgga aattgacgag gagcttcgtc gggcaaggga tttggtacca 1500
gagcacttga gagttcgctc tgtcgaagag acacaactgg atcccgcgaa ccttatcatg 1560
tctcggtttg agatcatgag tgtgtaccac aaagctcaat gcgttctcca tcggcgattc 1620
ctcgcgccgg cgcgcgaaaa ccctcgattt acctattctc gaagaacctg cattgattcg 1680
gctctggagc tactcgata tcagtcctatg attcataccg acaccgtcc caacggtcgt 1740
ctgcgaggga agctcaaccg gaccacgtcc ctctgttcga gcgactttct gcttgccgct 1800
accattgtgt gcctagatct ctatcatgga cttcagctac aagctggagg tcgcgcttca 1860
gatgacacct acacctgggg acgggagcgt cgcgacgaaa tggttgcggc tctacagcgc 1920
tcgaaggaga tctgggacga gcttcaagac gagaccatag acgcgtggaa ggcttcagga 1980
gtcctcggcg tgatgcttgc ccggtgaac ctacgacgga acaccgcttc gaccacgttc 2040
gaaccgcaag acgagaagca gagtgcgcgc atgacgttag gcctgcttag cagtggcatg 2100
aactatatga atccaggaac acctggcttt ggagaagcca caaccaagat ggcagataca 2160
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agcgccatgt tcggacagat gccagatatg caggtcaatt tggattggga cgcttgggac 2280
aactacattc aaaactctc gattgacttt tccaatcagt ggtggccgac tatggacgca 2340
cagcaagcgc cacagcctcc gcaaccaggg aaccgcgttt cgccatctca gttggtgca 2400
acacagggcg gaattgcagg aaggatgcgt acgatgcgt cgctttctag cgcattccca 2460
gaacccaatg ggtacgatgc ggctttccct acatccttca gcgtgaatgc gccgaaaaac 2520
ccacacaatc ctgcttcagg cccaggaaca 2550

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<210> 96

<211> 850

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 96

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Met Thr Pro Thr Pro Pro Ser Thr Thr Ser Ser Ser Ala Gly Gly Ile
 1          5          10          15
Ser Pro Glu Gly His Tyr Arg Val Ile Arg Lys Arg Asn Arg Val Pro
          20          25          30
Leu Ser Cys Gly Pro Cys Arg His Arg Lys Leu Lys Cys Asn Arg Ala
          35          40          45
His Pro Cys Glu Asn Cys Val Lys Arg Gly Asp Ala Ser Ser Cys Thr
          50          55          60
Tyr Ala Gln Ala Asn Ala Arg Lys Lys Asn Ser Pro Leu Gln Thr Ala
65          70          75          80
Ser Ser Ser Pro Asp Asp Met Gln Asn Arg Ile Asp Arg Leu Glu Ser
          85          90          95
Leu Val Leu Ser Leu Met Thr Asn Gly Ser Gln Ser Ala Gly Pro Thr
          100          105          110
Ala Ala Met Ala Val Ile Ser Gly Asn Ser Ser Ser Ile Gly Ser Ala

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Pro Asn Gly Arg Leu Arg Gly Lys Leu Asn Arg Thr Thr Ser Leu Cys  
 580 585 590  
 Ser Ser Asp Phe Leu Leu Ala Ala Thr Ile Val Cys Leu Asp Leu Tyr  
 595 600 605  
 His Gly Leu Gln Leu Gln Ala Gly Gly Arg Ala Ser Asp Asp Thr Tyr  
 610 615 620  
 Thr Trp Gly Arg Glu Arg Arg Asp Glu Met Val Ala Ala Leu Gln Arg  
 625 630 635 640  
 Ser Lys Glu Ile Trp Asp Glu Leu Gln Asp Glu Thr Ile Asp Ala Trp  
 645 650 655  
 Lys Ala Ser Gly Val Leu Gly Val Met Leu Ala Arg Leu Asn Leu Asp  
 660 665 670  
 Gly Asn Thr Ala Ser Thr Thr Phe Glu Pro Gln Asp Glu Lys Gln Ser  
 675 680 685  
 Ala Ala Met Thr Leu Gly Leu Leu Ser Ser Gly Met Asn Tyr Met Asn  
 690 695 700  
 Pro Gly Thr Pro Gly Phe Gly Glu Ala Thr Thr Lys Met Ala Asp Thr  
 705 710 715 720  
 Pro Val Pro Pro Pro Gly Gly Phe Gly Ala Ala Asp Met Pro Gly Ala  
 725 730 735  
 Pro Ser Pro Phe Ser Ala Met Phe Gly Gln Met Pro Asp Met Gln Val  
 740 745 750  
 Asn Leu Asp Trp Asp Ala Trp Asp Asn Tyr Ile Gln Asn Ser Ser Ile  
 755 760 765  
 Asp Phe Ser Asn Gln Trp Trp Pro Ala Met Asp Ala Gln Gln Ala Pro  
 770 775 780  
 Gln Pro Pro Gln Pro Gly Asn Pro Leu Ser Pro Ser Gln Leu Ala Ala  
 785 790 795 800  
 Thr Gln Gly Gly Ile Ala Gly Arg Met Arg Thr Met Pro Ser Leu Ser  
 805 810 815  
 Ser Ala Phe Pro Glu Pro Asn Gly Tyr Asp Ala Ala Phe Pro Thr Ser  
 820 825 830  
 Phe Ser Val Asn Ala Pro Lys Asn Pro His Asn Pro Ala Ser Gly Pro  
 835 840 845  
 Gly Thr  
 850

&lt;210&gt; 97

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 97

atgacaccgc gacaatcctc cccatccgaa cactcgcact ccgacaacaa tgtgcgcaag 60  
 cgcgatatgta aagcctgcga tcgctgtcgc ctgaaaaagt ccaagtgtga cggaggcaac 120  
 ccgtgcgggc ggtgtcgcgc agacaatgcc atctgcgtct ttggcgagcg caaaaaggcg 180  
 catgacaaag tgtaccccaa gggatacgtt gagatgcttg aacagcagca ggcctggctc 240  
 gtctacggcc tgcagggaact gtaccgccgc accagcgacg gcgaaggctg gcccggcgag 300  
 ccgctcaagt gcgaggccaa cggccaccgc ctcacgcacg acctgctcac ccgcctcggc 360  
 gccctcgacc aggccaaagg cgagcgcttc gaggaaaacc ccgacgccat gcagcaggag 420  
 ctctggcgcc agaacgccgg ccacatgcag cgccaggact cgtccgacgc cagctccgac 480  
 agcgcgccact cgcccgtcgt cccctccgtc gccgcgcgcg ccgcccgtcg cttcgccgac 540  
 cccttcgccc agccccagct gccccccacc ccgccaaata tcagccccag cgcccccccc 600

```

gtcaagtcg agtcgtcgca gatgccgccg gcctttgcgt ccgcgccgct gggcatgcag 660
ggcgctcgta accccatggg gctgcaggcg ccgcagcagc aacagcagca gcagcagtcg 720
tgggggagga atgggttcgg cgggttcgat gatatcgaca tgatgggcac gacggatttt 780
accaacctgt cgtttgacga tccgctgtcg tcgccgatgt tcaatcgacc cgtgccgatc 840
aactgcatgt cgtatatgga cttgaagggc gactacgacg atctgaacca gtttgtcaat 900
gcgaatgcgc cggagatcgc gtcgacg                                     927

```

&lt;210&gt; 98

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 98

```

Met Thr Pro Arg Gln Ser Ser Pro Ser Glu His Ser His Ser Asp Asn
 1          5          10          15
Asn Val Arg Lys Arg Val Cys Lys Ala Cys Asp Arg Cys Arg Leu Lys
      20          25          30
Lys Ser Lys Cys Asp Gly Gly Asn Pro Cys Gly Arg Cys Arg Ala Asp
      35          40          45
Asn Ala Ile Cys Val Phe Gly Glu Arg Lys Lys Ala His Asp Lys Val
      50          55          60
Tyr Pro Lys Gly Tyr Val Glu Met Leu Glu Gln Gln Gln Ala Trp Leu
      65          70          75          80
Val Tyr Gly Leu Gln Glu Leu Tyr Arg Arg Thr Ser Asp Gly Glu Gly
      85          90          95
Trp Pro Gly Glu Pro Leu Lys Cys Glu Ala Asn Gly His Pro Leu Thr
      100         105         110
His Asp Leu Leu Thr Arg Leu Gly Ala Leu Asp Gln Ala Lys Gly Glu
      115         120         125
Arg Phe Glu Glu Asn Pro Asp Ala Met Gln Gln Glu Leu Trp Arg Gln
      130         135         140
Asn Ala Gly His Met Gln Arg Gln Asp Ser Ser Asp Ala Ser Ser Asp
      145         150         155         160
Ser Ala His Ser Pro Val Val Pro Ser Val Ala Ala Ala Ala Ala Ala
      165         170         175
Arg Phe Ala Asp Pro Phe Ala Gln Pro Gln Leu Pro Pro Thr Pro Pro
      180         185         190
Asn Ile Ser Pro Ser Ala Arg Pro Val Lys Ser Glu Ser Ser Gln Met
      195         200         205
Pro Pro Ala Phe Ala Ser Ala Pro Leu Gly Met Gln Gly Val Val Asn
      210         215         220
Pro Met Val Leu Gln Ala Pro Gln Gln Gln Gln Gln Gln Gln Ser
      225         230         235         240
Trp Gly Gly Asn Gly Phe Gly Gly Phe Asp Asp Ile Asp Met Met Gly
      245         250         255
Thr Thr Asp Phe Thr Asn Leu Ser Phe Asp Asp Pro Leu Ser Ser Pro
      260         265         270
Met Phe Asn Arg Pro Val Pro Ile Asn Cys Met Ser Tyr Met Asp Leu
      275         280         285
Lys Gly Asp Tyr Asp Asp Leu Asn Gln Phe Val Asn Ala Asn Ala Pro
      290         295         300
Glu Ile Ala Ser Thr
305

```

<210> 99  
 <211> 1374  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 99  
 atgctctgtc acatcatgac agtgggtaca cccgctgtga cgcaagtcca tgaaaatggc 60  
 ctgaacggac atgtcccaca tcaacatcac caccaccacc atcatccgca ccaaaccaat 120  
 gtgaacctgc ctcggtttca cccaatcgcc atgaaccgga gccagccagt ccatccagag 180  
 cacatggccg tgccaaatca tcctcacttt cgcccatttc cgccgcccgc gccaatgcat 240  
 gaaccggggc cgcctccccc ggggggtcat cccgccata tagatcatat cgaagctcga 300  
 ctgaggcagt tggagcatga ggaagccgct cgcattggcg ctcgtagtca actactcgca 360  
 atccgcaagc gggaagacga agaattccgt aggatgaccg agaacgctga agcgggaagaa 420  
 gaggaactac gtagacagcg gaaacgcctg aagcgcgagt ccatgggtct ggggttcaat 480  
 gccaccggtg actcgcctcc cctacgtccc acgcccctc gccggctatc agaaacaaac 540  
 gcagccacca ctctggcctt cttcaagcaa caaagcccgc cagagccacg accgattccc 600  
 gtgcaggcgc cgccgcacca cccgccaccg cctccgcagc atctgcacga ctcgacgggg 660  
 gccaccatcc gccgcaagca gaaatacacg atcaaaaacg tcgaagcatg gggcgagcgc 720  
 caccgcccgc ccgcggcgca cgaccgcgtc ggccgcgcgc tgtggaagcg gccctccgac 780  
 ggcagccctg tgtacctcac ctgcccgggt tggggctgcg gcaaggccga ctttgtcacg 840  
 ctgcacgggt tcatgtgcc a tctgaccaag aagcacaagg accgcagcct gggcagccag 900  
 tcgcgcgcgc tggaagtctg cggcatcgtc tacgacccca acgcccgcgt gccgcccgtg 960  
 gccgcccgtg cccgcgcctc caccgaggag agcgcctcg agtcgccgca ccgggacggc 1020  
 tatccgcagg agatggacac gtcttcggta tcggacgagg agcagcgcga gcacaccgtc 1080  
 aagaccgagt ccaccgagag atcgttgccg gcgcacgcgc cgcccttccc gccccccgac 1140  
 gagcccgta aagcatccc tctcaacggc tccacgaaac agaccatctc gtccatcatc 1200  
 gaccgcgagc cggacgatga gccgcgcgag cggcccgcct ccatccccc cgtccagccc 1260  
 gagtccggcg tcctgccttc cccggagcag aagtcggtcg ttcgggagga ggagcccaag 1320  
 tcggcggata gcgaaaagga aaatacggag ccgaaagacg tgtcggaac aaag 1374

<210> 100  
 <211> 458  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 100  
 Met Leu Cys His Ile Met Thr Val Ala Thr Pro Ala Val Thr Gln Val  
 1 5 10 15  
 His Glu Asn Gly Leu Asn Gly His Val Pro His Gln His His His His  
 20 25 30  
 His His His Pro His Gln Thr Asn Val Asn Leu Pro Arg Phe His Pro  
 35 40 45  
 Ile Ala Met Asn Pro Ser Gln Pro Val His Pro Glu His Met Ala Val  
 50 55 60  
 Pro Asn His Pro His Phe Arg Pro Phe Pro Pro Pro Pro Met His  
 65 70 75 80  
 Glu Pro Gly Pro Pro Pro Gly Ala His Pro Ala His Ile Asp His  
 85 90 95  
 Ile Glu Ala Arg Leu Arg Gln Leu Glu His Glu Glu Ala Ala Arg Met  
 100 105 110



Ala Ala Arg Ser Gln Leu Leu Ala Ile Arg Lys Arg Glu Asp Glu Glu  
 115 120 125  
 Phe Arg Arg Met Thr Glu Asn Ala Glu Ala Glu Glu Glu Glu Leu Arg  
 130 135 140  
 Arg Gln Arg Lys Arg Leu Lys Arg Glu Ser Met Gly Leu Gly Phe Asn  
 145 150 155 160  
 Ala Thr Val Asp Ser Pro Pro Leu Arg Pro Thr Pro Pro Arg Arg Leu  
 165 170 175  
 Ser Glu Thr Asn Ala Ala Thr Thr Leu Ala Phe Phe Lys Gln Gln Ser  
 180 185 190  
 Pro Pro Glu Pro Arg Pro Ile Pro Val Gln Ala Pro Pro His His Pro  
 195 200 205  
 Pro Pro Pro Pro Gln His Leu His Asp Ser Thr Gly Ala Thr Ile Arg  
 210 215 220  
 Arg Lys Gln Lys Tyr Thr Ile Lys Asn Val Glu Ala Trp Gly Glu Arg  
 225 230 235 240  
 His Gly Arg Pro Ala Ala His Asp Pro Ser Gly Arg Ala Leu Trp Lys  
 245 250 255  
 Arg Pro Ser Asp Gly Ser Leu Val Tyr Leu Thr Cys Pro Val Ser Gly  
 260 265 270  
 Cys Gly Lys Ala Asp Phe Val Thr Leu His Gly Phe Met Cys His Leu  
 275 280 285  
 Thr Lys Lys His Lys Asp Arg Ser Leu Gly Ser Gln Ser Arg Ala Leu  
 290 295 300  
 Glu Val Cys Gly Ile Val Tyr Asp Pro Asn Ala Pro Leu Pro Pro Val  
 305 310 315 320  
 Ala Ala Val Pro Arg Ala Ser Thr Glu Glu Ser Arg Leu Glu Ser Pro  
 325 330 335  
 His Pro Asp Gly Tyr Pro Gln Glu Met Asp Thr Ser Ser Val Ser Asp  
 340 345 350  
 Glu Glu Gln Arg Glu His Thr Val Lys Thr Glu Ser Thr Glu Arg Ser  
 355 360 365  
 Leu Pro Ala His Ala Ala Pro Phe Pro Pro Pro Asp Glu Pro Val Lys  
 370 375 380  
 Ala Ser Arg Leu Asn Gly Ser Thr Lys Gln Thr Ile Ser Ser Ile Ile  
 385 390 395 400  
 Asp Arg Glu Pro Asp Asp Glu Pro Arg Glu Arg Pro Ala Ser Ile Pro  
 405 410 415  
 Pro Val Gln Pro Glu Ser Ala Val Leu Pro Ser Pro Glu Gln Lys Ser  
 420 425 430  
 Val Val Arg Glu Glu Glu Pro Lys Ser Ala Asp Ser Glu Lys Glu Asn  
 435 440 445  
 Thr Glu Pro Lys Asp Val Ser Glu Thr Lys  
 450 455

&lt;210&gt; 101

&lt;211&gt; 1728

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 101

atgaacgatac ctttcgtccc cgcaaaaaat cccggcccgga cgaaagccgc gggtcacctg 60  
 ctgttgacct gtcttctgtg ccgtcacaaa cacctcaaat gtgatgggaa aactccagt 120

```

tgcggacgct gtgccgctac tggatcgga tgcgaatata ccccgctcgcg tcgtgggtac 180
aagggcccggt cgaagaagcg acgcgcaaac ccgtcgtctc cagagcaaac gcccgccgat 240
ctggccgcct cgttcgatcc gcagtcacac ggtttggtca atgtcacccc tgactggagc 300
ctgcaaaaca cggtcctctt catgcccgtc gctaccttcc cgtcctcctc gtcgaccagc 360
ccgggcttga ccgactacac caattcttcg caaccatcc gggtcacgaa tgacccctta 420
actcccgact cttccgcctc ggtccccggt gatgggtatt tgatcgatat ctactatacc 480
tatttccatc cctcgcaccc aattctccct ccgctccgct ttctctaccg ctctatctc 540
ccgaccttcc tggagcaggt catcaagttc atcggtgctc atttactcc ggccgcttcg 600
agcgagacgt atcgaccac cgttgtgtca aatgtgaagg agcaagagg ctctatagag 660
aagctgcagg ctctcttgtt gctcgcggtg gtcctccact ctcgcaatga acgtccgaa 720
gctggcgagt gtctcgcggt agctgttgac ctacggttg agctgggact ccagacgag 780
agtttcgcca ccgcgatgag cgacggtgac cccatccgcg cggaatgcct gcggcgaca 840
tggtgggagc tgttcattat cgaggggatg ctgactgcac ttgggggttca gagcacttac 900
cgtaccaaca tgggtgcgccc ggaggtggga ctaccatgtg aggaacggat ctaccaggat 960
ggcttggcgc cgccccgcgc tccaacgata gctcaattcg acaatcgcgt cttcgccgac 1020
gaggagcgcg acttctcttc cttcacctac cgtatcgagg cggtcgcgat tctcgggcgc 1080
gtggtcggca tccaggacat ggtcgagggc caacaggacc atgtggaggc cattgacgcc 1140
cgaatcacga gttggttcca ccacctccc gagtccaagg cggagctgct gcgtcccgat 1200
ggttccgtgg atgagatgat gttccaagcc accatgatcg tgaacggcgc gtcgatatac 1260
ctccacttcc cccgttctga tttgtgtgca tcgccgcca tggccgcgga agtgatctgc 1320
ggtcaccacg gacctgcag cattcccga ttttcacacc acgcccacgc aatgaaggcc 1380
ctcaaagccg ccagcgagat ctctcgtctg gcttccatcc gcatgccggt ggtcaaacac 1440
acgcccttct tcatctgcgc cctgggttatg agctcgatcg tgcagctggc tgcagtctcc 1500
gtcaaggccg ggcagatgcc cgatcccagc cgggatcgcc tcaccctgac cattggcgtc 1560
ttcaaatccc tggcccgcac gtgggccatc tccagacaa tcatgaggca gatcaaagcc 1620
gtgtcgcgcg atgttatgga catgggactg cggccggcca tggaccagat tgatctgacg 1680
accctcctcg atagcggctc gttcttcatg cccgatggac tgatgcga 1728

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<210> 102

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 102

```

Met Asn Asp Pro Phe Val Pro Ala Lys Asn Pro Gly Pro Thr Lys Ala
 1             5             10             15
Ala Gly Pro Ser Leu Leu Ala Cys Leu Leu Cys Arg His Lys His Leu
      20             25             30
Lys Cys Asp Gly Lys Thr Pro Val Cys Gly Arg Cys Ala Ala Thr Gly
      35             40             45
Ser Glu Cys Gln Tyr Thr Pro Ser Arg Arg Gly Tyr Lys Gly Pro Ser
      50             55             60
Lys Lys Arg Arg Ala Asn Pro Ser Ser Pro Glu Gln Thr Pro Ala Asp
      65             70             75             80
Leu Ala Ala Ser Phe Asp Pro Gln Ser Ile Gly Leu Val Asn Val Thr
      85             90             95
Pro Asp Trp Ser Leu Gln Asn Thr Val Pro Phe Met Pro Val Ala Thr
      100            105            110
Phe Pro Ser Ser Ser Thr Ser Pro Gly Leu Thr Asp Tyr Thr Asn
      115            120            125
Ser Ser Gln Pro Ile Arg Phe Thr Asn Asp Pro Leu Thr Pro Asp Ser
      130            135            140
Ser Ala Ser Val Pro Gly Asp Gly Tyr Leu Ile Asp Ile Tyr Tyr Thr
      145            150            155            160

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Tyr Phe His Pro Ser His Pro Ile Leu Pro Pro Leu Arg Phe Leu Tyr
      165      170      175
Arg Ser Tyr Leu Pro Thr Phe Leu Glu Gln Val Ile Lys Phe Ile Gly
      180      185      190
Ala His Phe Thr Pro Ala Ala Ser Ser Glu Thr Tyr Arg Pro Thr Val
      195      200      205
Val Ser Asn Val Lys Glu Gln Glu Gly Ser Ile Glu Lys Leu Gln Ala
      210      215      220
Leu Leu Leu Leu Ala Val Val Leu His Ser Arg Asn Glu Arg Pro Glu
225      230      235      240
Ala Gly Glu Cys Leu Ala Gly Ala Val Asp Leu Ala Phe Glu Leu Gly
      245      250      255
Leu Gln Thr Gln Ser Phe Ala Thr Ala Met Ser Asp Gly Asp Pro Ile
      260      265      270
Arg Ala Glu Cys Leu Arg Arg Thr Trp Trp Glu Leu Phe Ile Ile Glu
      275      280      285
Gly Met Leu Thr Ala Leu Gly Val Gln Ser Thr Tyr Arg Thr Asn Met
      290      295      300
Val Pro Pro Glu Val Gly Leu Pro Cys Glu Glu Arg Ile Tyr Gln Asp
305      310      315      320
Gly Leu Ala Pro Pro Pro Pro Pro Thr Ile Ala Gln Phe Asp Asn Arg
      325      330      335
Val Phe Ala Asp Glu Glu Arg Asp Phe Ser Ser Phe Thr Tyr Arg Ile
      340      345      350
Glu Ala Val Arg Ile Leu Gly Arg Val Val Gly Ile Gln Asp Met Val
      355      360      365
Glu Gly Gln Gln Asp His Val Glu Ala Ile Asp Ala Arg Ile Thr Ser
      370      375      380
Trp Phe His His Leu Pro Glu Ser Lys Ala Glu Leu Leu Arg Pro Asp
385      390      395      400
Gly Ser Val Asp Glu Met Met Phe Gln Ala Thr Met Ile Val Asn Gly
      405      410      415
Ala Ser Ile Tyr Leu His Phe Pro Arg Ser Asp Leu Leu Ser Ser Pro
      420      425      430
Ala Met Ala Ala Glu Val Ile Cys Gly His His Gly Pro Cys Ser Ile
      435      440      445
Pro Ala Phe Ser His His Ala His Ala Met Lys Ala Leu Lys Ala Ala
      450      455      460
Ser Glu Ile Ser Ser Leu Ala Ser Ile Arg Met Pro Val Val Lys His
465      470      475      480
Thr Pro Phe Phe Ile Cys Ala Leu Val Met Ser Ser Ile Val Gln Leu
      485      490      495
Ala Ala Cys Ser Val Lys Ala Gly Gln Met Pro Asp Pro Ser Arg Asp
      500      505      510
Arg Leu Thr Leu Thr Ile Gly Val Phe Lys Ser Leu Ala Arg Thr Trp
      515      520      525
Ala Ile Ser Gln Thr Ile Met Arg Gln Ile Lys Ala Val Ser Arg Asp
      530      535      540
Val Met Asp Met Gly Leu Arg Pro Ala Met Asp Gln Ile Asp Leu Thr
545      550      555      560
Thr Leu Leu Asp Ser Gly Arg Phe Leu Met Pro Asp Gly Leu Met Arg
      565      570      575

```

<210> 103  
 <211> 1272  
 <212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 103

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atggccaaac ccaaccagcg ccatgcctgt gaccgctgtc acggtcaaaa actgcgatgc 60
atccactccg ggggtgggccc gtgtgtacgc tgcgccaaag ccaaagccac ctgcagctgg 120
agccagtcct tacgttccaa ccgactcaag agacataacg cgcgatatac tgatgttcct 180
ttggcgtgtg cgcaactagc aaccagtcg accgacccaa acacacctca atttggtgca 240
tacatgagcc aacctctctc cgcggcggtt gacattgaca tcaacttgct gcagactcaa 300
ttcacgcgaca gtactccctg ggctctgcgg gccggcgctt atccctctcc agcatcacag 360
gaaatggaga cttacaatgt gggtcacact gagggcgacc ttccggccac cgcggactgg 420
atgtggcccc cgctcgccaa tgggtccggt caaacgactc ccccgccaaa ttggcagcaa 480
gcattcaatc aggaatgggc tatgatggcg tcgcagcacc ctgtcgcaac gatggacacg 540
ccgtctcgga catcgccagt aagcgacgcc gtggaccgcg cgaagacggt gtgccttctt 600
gcgaccatcc gcgagttgtc agagcttaac gtcgacctgt acgcacacga agcgacggtc 660
cccagacctc ctgcatctct ggaggaaccg atcagctgga agaacaagga tttcgccatc 720
gatcggactt tccactgtc ccagcggctc attgagatcg tcaacaaacg atatccgcgc 780
tacctcgaga cggcccgcat gcagaccccg gaggggactc ccgaacggac ctccgaaagc 840
agtctgtctg gcccgccact tgaccaaggc tcatgtctcc tcgttctctc atgttacact 900
cgactcatcg agacctacga tcgaatcttt gccaatatgc agggatgtct ggatcgttcc 960
tcggtcacgg cccgagaaga ctacgtcaat atgccgtcgg tccaagtcgg ctcttctctc 1020
ttgccacact cgtcctcgtt gcaaatcgtc ctcatcctgc agttggcgcg tcaactccta 1080
actcgaatgg gcgagatcat caaagccggt cagccggaga aaagaactaa ccccgctgat 1140
gtcaccttgt ccgaatccgc aaccgggggt ctctactgt ctagecgttt ggagaccgtc 1200
tccgccgaag aagaccgtct gatgaaaaga atcacgaaac tacgaagcac cttgattgag 1260
ctaaacattc tg                                     1272

```

<210> 104

<211> 424

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 104

```

Met Ala Lys Pro Asn Gln Arg His Ala Cys Asp Arg Cys His Gly Gln
 1           5           10           15
Lys Leu Arg Cys Ile His Ser Gly Gly Gly Pro Cys Val Arg Cys Ala
 20           25           30
Lys Ala Lys Ala Thr Cys Ser Trp Ser Gln Ser Leu Arg Ser Asn Arg
 35           40           45
Leu Lys Arg His Asn Ala Pro Ile Ser Asp Val Pro Leu Ala Cys Ala
 50           55           60
Gln Leu Ala Thr Gln Ser Thr Asp Pro Asn Thr Pro Gln Phe Gly Ala
 65           70           75           80
Tyr Met Ser Gln Pro Ser Ser Ala Gly Val Asp Ile Asp Ile Asn Leu
 85           90           95
Leu Gln Thr Gln Phe Thr Asp Ser Thr Pro Trp Ala Leu Pro Ala Gly
100           105           110
Arg Tyr Pro Ser Pro Ala Ser Gln Glu Met Glu Thr Tyr Asn Val Gly
115           120           125
His Thr Glu Ala Asp Leu Pro Ala Thr Ala Asp Trp Met Trp Pro Ala
130           135           140
Val Ala Asn Gly Pro Val Gln Thr Thr Pro Pro Ala Asn Trp Gln Gln

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145          150          155          160
Ala Phe Asn Gln Glu Trp Ala Met Met Ala Ser Gln His Pro Val Ala
          165          170          175
Thr Met Asp Thr Pro Ser Arg Thr Ser Pro Val Ser Asp Ala Val Asp
          180          185          190
Pro Pro Lys Thr Val Cys Leu Leu Ala Thr Ile Arg Glu Leu Ser Glu
          195          200          205
Leu Asn Val Asp Leu Tyr Ala His Glu Ala Thr Val Pro Arg Pro Pro
          210          215          220
Ala Ser Leu Glu Glu Pro Ile Ser Trp Lys Asn Lys Asp Phe Ala Ile
225          230          235          240
Asp Arg Thr Phe His Leu Ser Gln Arg Leu Ile Glu Ile Val Asn Lys
          245          250          255
Arg Tyr Pro Arg Tyr Leu Glu Thr Ala Arg Met Gln Thr Pro Glu Gly
          260          265          270
Thr Pro Glu Arg Thr Ser Glu Ser Ser Leu Ser Gly Pro Pro Leu Asp
          275          280          285
Gln Gly Ser Cys Leu Leu Val Leu Ser Cys Tyr Thr Arg Leu Ile Glu
          290          295          300
Thr Tyr Asp Arg Ile Phe Ala Asn Met Gln Gly Cys Leu Asp Arg Ser
305          310          315          320
Ser Val Thr Ala Arg Glu Asp Tyr Val Asn Met Pro Ser Val Gln Val
          325          330          335
Gly Ser Phe Ser Leu Pro His Ser Ser Ser Leu Gln Ile Val Leu Ile
          340          345          350
Leu Gln Leu Ala Arg Gln Leu Leu Thr Arg Met Gly Glu Ile Ile Lys
          355          360          365
Ala Val Gln Pro Glu Lys Arg Thr Asn Pro Ala Asp Val Thr Leu Ser
          370          375          380
Glu Ser Ala Thr Gly Gly Leu Leu Leu Ser Ser Ala Leu Glu Thr Val
385          390          395          400
Ser Ala Glu Glu Asp Arg Leu Met Lys Arg Ile Thr Lys Leu Arg Ser
          405          410          415
Thr Leu Ile Glu Leu Asn Ile Leu
          420

```

&lt;210&gt; 105

&lt;211&gt; 1473

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 105

```

atggagacgt attacgggca cgttcgcaaca cctgcggacg ctattattct ttttgaggct 60
tgccgtatcg gcctttttacc tcgcgtgcaa agacgattat cagagaaaga gagacaatca 120
atccgttccg gttcgggtctt tgtatgggat gagcgagaag cgggtatgcg gcatgggacc 180
gatgggaagt catggagcgc cagccgtgtg tctggtagct ttttgacgta tcgtgaaatg 240
gaaggcaagc gtggagggtg tagcgtctct cagggttctg cgtcccaggg aggtaaaacg 300
cctgagagtc ggggcagtga cgatgatcgt gcggtaggaa cagatgaggg accagatggg 360
taccgttaca aaccagatgg cttgatgaag cagcttttca gtatcacaac ctccaacggt 420
caacatctgc atctcattag ctactattca cgatctcacc cttcggccgc caacttaca 480
caaccaacta cggatcctgc gctacgccat gttcgccccc agaaaggcct ctatcccgag 540
tcaacagtca acgatcagca aaacctccct gtcgttacct gtggacctat gcaaggcgct 600
gcgtacccca taactccca tcctctcggc gcataccgcg gcgtcactca tacacagcca 660

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tatccacctg cctatgcttg gccgccacc cctctagcca caccaccgac tgtctcggtt 720
caatacggcc ctggtccttc ttatctgccc ccggtagggtg ccaatggaca tcctcattat 780
ggcccgccac atcatcagcc tccacctcat caacatggcg gtggactacc accccctcca 840
cacgggatga caagcccgtg tgatcgacca cctcacaatg aatcaacatt gcctccagct 900
ggaccaccgt cacaacagcc aagctacatg aaccggtcac cgcgctcaat acacgaccat 960
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gctgaggggtc cacgggatat ccctaacgag aagatcagat tcggaggcga ggacacgag 1440
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<210> 106

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 106

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Leu Ser Glu Lys Glu Arg Gln Ser Ile Arg Ser Gly Ser Val Phe Val
      35           40           45
Trp Asp Glu Arg Glu Ala Gly Met Arg Arg Trp Thr Asp Gly Lys Ser
      50           55           60
Trp Ser Ala Ser Arg Val Ser Gly Ser Phe Leu Thr Tyr Arg Glu Met
      65           70           75           80
Glu Gly Lys Arg Gly Gly Gly Ser Val Ser Gln Gly Ser Ala Ser Arg
      85           90           95
Gly Gly Lys Thr Pro Glu Ser Arg Gly Ser Asp Asp Asp Arg Ala Asp
      100          105          110
Gly Thr Asp Glu Gly Pro Asp Gly Tyr Arg Tyr Lys Pro Asp Gly Leu
      115          120          125
Met Lys Gln Ser Phe Ser Ile Thr Thr Ser Asn Gly Gln His Leu His
      130          135          140
Leu Ile Ser Tyr Tyr Ser Arg Ser His Pro Ser Ala Ala Asn Leu Gln
      145          150          155          160
Gln Pro Thr Thr Asp Pro Ala Leu Arg His Val Arg Pro Gln Lys Gly
      165          170          175
Leu Tyr Pro Glu Ser Thr Val Asn Asp Gln Gln Asn Leu Pro Val Val
      180          185          190
Thr Arg Gly Pro Met Gln Gly Ala Tyr Pro Ile Thr Pro His Pro
      195          200          205
Leu Gly Ala Tyr Pro Arg Val Thr His Thr Gln Pro Tyr Pro Pro Ala
      210          215          220
Tyr Ala Trp Pro Pro Thr Pro Leu Ala Thr Pro Pro Thr Val Ser Val
      225          230          235          240
Gln Tyr Gly Pro Gly Pro Ser Tyr Leu Pro Pro Val Gly Ala Asn Gly
      245          250          255
His Pro His Tyr Gly Pro Pro His His Gln Pro Pro Pro His Gln His

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Gln	Gln	Pro	Ser	Tyr	Met	Asn	Arg	Ser	Pro	Arg	Ser	Ile	His	Asp	His	
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Ala	Gln	Ala	His	Ala	His	Ala	His	Ala	His	Ala	Gln	Ala	Gln	Ala	Gln	
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Ala	Gln	Ala	Gln	Ala	Gln	Ala	Gln	Ala	Gln	Ala	Gln	Ala	His	Ala	His	
			340				345						350			
Glu	Gln	Arg	Thr	Pro	Pro	Val	Tyr	Gly	His	Pro	Leu	Val	Asp	Pro	Arg	
		355					360					365				
Met	Ala	Ser	Pro	Arg	Val	Pro	Val	Gln	Ser	Leu	Ala	Gln	Pro	Asn	Gly	
	370					375					380					
His	Ala	His	Ser	Pro	His	Leu	Ala	Lys	Gln	Glu	His	Pro	Ala	Ala	Leu	
385					390					395					400	
Pro	Ser	Leu	Asn	Pro	Ile	Ala	Ala	Ser	Pro	Lys	Ser	Ser	Asp	Pro	Ala	
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Ser	Ala	Gly	Asn	Ala	Val	Pro	Gly	Ile	Gly	Ser	Leu	Met	Asn	Gly	Ala	
			420				425						430			
Gly	Leu	Ala	Pro	Leu	Ser	Ser	Ser	Thr	Ala	Ser	Pro	Gly	Gly	Pro	Ala	
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Ala	Ser	Ser	Asn	Gly	Thr	Pro	Ala	Ala	Ser	Ser	Phe	Ala	Glu	Gly	Pro	
		450				455					460					
Arg	Asp	Ile	Pro	Asn	Glu	Lys	Ile	Arg	Phe	Gly	Gly	Glu	Asp	Thr	Arg	
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Ala	Leu	Arg	Gln	Leu	Asp	Arg	Ala	Phe	Ile	Ala						
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<210> 107

<211> 2577

<212> DNA

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> fungal gene

<400> 107

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cagcaatcat	ctactacacc	ggatgatatg	caaaaccgca	tcgatcgggt	agaaggcttg	300
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atttcagggt	aaagtatgtc	gggctccacc	cggttctccc	atgacctcga	cgccgaagag	420
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atgaagatgg	acaattacaa	gtcctattac	atcagtgacg	ctcatggggc	gtctgtattg	540
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ggcgacgagc	caccgcaatt	ccggggcaag	tcctttggaca	tggccggcgg	attccgaaat	960
ttctgtagcac	agtgcctgac	attggctgac	tacacgaaac	ccaccocctt	cttgattgag	1020

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gcgcttgtat ttcacttgca tggcgatttc tctctgaccc gagaggcgga catctccatc 1080
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ataccgacaa tgtactcagc atcctccaac agtcccagata gtgcagggtg gccagtgaca 2520
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<210> 108

<211> 859

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 108

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      20           25           30
Arg Asn Arg Val Pro Leu Ser Cys Gly Pro Cys Arg His Arg Lys Leu
      35           40           45
Lys Cys Asn Arg Thr His Pro Cys Glu Asn Cys Val Lys Arg Gly Asp
      50           55           60
Ala Ala Ser Cys Asn Tyr Ala Gln Pro Asn Ser Arg Lys Lys Asn Pro
65           70           75           80
Gln Gln Ser Ser Thr Thr Pro Asp Asp Met Gln Asn Arg Ile Asp Arg
      85           90           95
Leu Glu Gly Leu Val Leu Ser Leu Met Thr Asn Gly Ser Gln Ser Ala
      100          105          110
Gly Pro Asn Ala Ala Met Ala Ala Ile Ser Gly Glu Ser Ser Ala Gly
      115          120          125
Ser Thr Arg Phe Ser His Asp Leu Asp Ala Glu Glu Glu Gly Met Glu
      130          135          140
Gly Ala Glu Glu Ser Asp Thr Asp Gln Val Thr Lys Ser Phe Gly Ile
145          150          155          160
Met Lys Met Asp Asn Asn Lys Ser Tyr Tyr Ile Ser Asp Ala His Trp

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Thr Trp Gly Arg Glu Arg Arg Asp Glu Met Thr Ala Ala Ile Gln His  
 625 630 635 640  
 Ser Lys Glu Ile Trp Asp Glu Ser Arg Asp Glu Ser Met Glu Ala Trp  
 645 650 655  
 Lys Ala Ser Thr Val Leu Gly Val Met Leu Ser Lys Leu His Met Thr  
 660 665 670  
 Val Pro Gly Leu Glu Asn Ser Ala Gly Ala Ala Ser Phe Glu Pro Gln  
 675 680 685  
 Asp Glu Lys Gln Asn Ala Ala Met Thr Leu Gly Leu Leu Ser Ser Gly  
 690 695 700  
 Met Ser Pro Met Asn Pro Gly Gln Pro Pro Phe Ala Asp Pro Met Phe  
 705 710 715 720  
 Lys Met Gly Asp Ser Pro Met Gly Thr Gly Thr Gly Ala Val Gly Ala  
 725 730 735  
 Ser Ala Glu Met Pro Gly Ala Leu Ser Pro Phe Ser Ser Met Phe Gly  
 740 745 750  
 Gln Met Pro Asp Met Gln Val Asn Leu Asp Trp Asp Ala Trp Asp Thr  
 755 760 765  
 Tyr Ile Gln Asn Pro Thr Leu Asp Thr Thr Asn Gln Phe Trp Pro Met  
 770 775 780  
 Met Asp Ala Gln Arg Gln Ala Thr Pro Gln Ser Gly Gly Met Ser Gln  
 785 790 795 800  
 Pro Ser Val Ser Ser Pro Leu Ala Ser Gly Arg Val Pro Ser Ile Ser  
 805 810 815  
 Gly Val Pro Arg Ile Pro Thr Met Tyr Ser Ala Ser Ser Asn Ser Pro  
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 Asp Ser Ala Gly Val Pro Val Thr Gly Tyr Gly Met Thr Pro Met Pro  
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&lt;210&gt; 109

&lt;211&gt; 3732

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 109

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 ggcacctata ccggttggcg cgccgaagtg cccatgaaag agcgcgtggt tcgagtgtat 180  
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 caagccatgg ccatggggat gaccgatccg aatcaacagg ccgccatgcc gcagcgatcg 540  
 caacagcagc aagccatgat gcagcagcag cagcaacaac agcaacaaca gcaacagcag 600  
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<210> 110

<211> 1244

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 110

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Val	Ala	Gln	Ala	Leu	His	Ala	Gln	Gly	Thr	Tyr	Thr	Gly	Trp	Arg	Ala
	35					40						45			
Glu	Val	Pro	Met	Lys	Glu	Arg	Val	Val	Arg	Val	Tyr	Gln	Met	Phe	Thr
	50				55						60				
Ser	Leu	Arg	Leu	Ile	Gln	Pro	Gln	Ala	Asp	Leu	Gln	His	Leu	Ala	Gln
65				70						75					80
Ala	Ala	Leu	Ser	Phe	Glu	Gln	Lys	Ala	Phe	Lys	Asp	Ala	Gln	Gln	Lys
			85						90					95	
Val	Asp	Tyr	Asp	Lys	Glu	Cys	Asn	Asp	Lys	Leu	Leu	His	Ile	Arg	Asp
		100						105					110		
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	115						120					125			
Gly	Ala	Pro	Lys	Ala	Gly	Gly	Met	Arg	Gly	Val	Gly	Gln	Pro	Ser	Phe
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Gln	Ala	Met	Ala	Met	Gly	Met	Thr	Asp	Pro	Asn	Gln	Gln	Ala	Ala	Met
			165					170						175	
Pro	Gln	Arg	Ser	Gln	Gln	Gln	Gln	Ala	Met	Met	Gln	Gln	Gln	Gln	Gln
		180						185					190		
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Arg	Ala
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Gln	Gln	Arg	Ser	Ala	Asn	Thr	Leu	Ala	Leu	Val	Asp	Glu	Leu	Asn	Asn
	210				215						220				
Leu	Thr	Pro	Gln	Glu	Tyr	Glu	Asn	Val	Asn	Arg	Val	Ala	His	Gln	Ile
225				230						235					240
Met	Thr	Lys	Thr	Ser	Pro	Val	Asp	Ala	Glu	Lys	Ile	Lys	Arg	Asn	Leu
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Asp	Pro	Val	Ala	Tyr	Phe	Phe	Arg	Ser	Gln	Ala	Leu	Ala	His	Leu	Lys
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Arg	Gln	Met	Lys	Ala	Arg	Val	Asp	Met	Ser	His	Pro	Gln	Asn	Thr	Gly
	290				295						300				
Val	Asp	Pro	Asn	Asn	Val	Met	Met	Gly	Ala	Asp	Pro	Thr	Met	Asn	Pro
305				310						315					320
Gln	Met	Phe	Pro	Asn	Met	Met	Asn	Leu	Gln	Arg	Asn	Ser	Ala	Phe	Ala
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	435						440					445			
Gln	Ala	Gln	Ala	Arg	Ala	Gln	Ala	Ala	Gln	Lys	Ala	Gln	Met	Ala	Ile

450		455		460
Ser Gln Ala Gly Gln	Ala Asn Ser His Leu Gln Gln Pro Met Pro Gln			
465	470	475		480
Gln Ser Pro Ala Met	Pro Met Leu Asn Arg Pro Met Pro Pro Gly Gln			
	485	490		495
Met Ser Pro Ala Gln	Met Ala Ala Gln Val Arg Pro Pro Ser Arg Ala			
	500	505		510
Pro Ala Met Gly Gln	Gln Pro Ser Met Gly Gly Gln Gln Pro Met Gln			
	515	520		525
Gly Arg Pro Gln Ile	Pro Pro Gly Leu Pro Pro Ala Ile Gln Glu Gln			
	530	535		540
Leu Ala Gln Met Ser	Pro Glu Gln Leu Asn Arg Val Leu Ala Gln Arg			
545	550	555		560
Arg Ala Met Ala Asn	Asn Pro Ala Leu Ala Arg Ala Asn Ala Ala Arg			
	565	570		575
Gln Ser Val Pro Met	Gln Gln Ser Val Ser Gln Ser Ala Gln Ala Gln			
	580	585		590
Ser Met Ala Asn Asn	Gln Asn Met Arg Ala Met Asn Val Gln Ala Gln			
	595	600		605
Leu Ala Gly Met Gly	Gly Ala Gln Gln Met Met Pro Gly Gln Gln Met			
	610	615		620
Ser Leu Gln Gln Gln	Gln Gln Gln Gln Gln Gln Gln Arg Gln Glu			
625	630	635		640
Leu Tyr Lys Met Gln	Leu Leu Gln Gln Ser Gly Gly Asn Leu Glu Leu			
	645	650		655
Ser Asn Glu Gln Ser	Lys Glu Met Asp Arg Leu His Phe Pro Pro Ser			
	660	665		670
Leu Leu Gly Asn Asn	Pro Asn Ile Val Ser Leu Val Pro Lys Asn Ile			
	675	680		685
Lys Thr Trp Gly Gln	Leu Lys Gln Trp Ala Ala Thr Asn Pro Gln Leu			
	690	695		700
Pro Gly Gly Leu Asn	Leu Gln Lys Leu Met Ala Leu Gln Lys Phe His			
705	710	715		720
Phe Thr Gln Ile Leu	Asn Gln Ser Lys Glu Arg Ser Arg Asn Pro Asp			
	725	730		735
Gln Ala Gly Gln Gly	Pro Trp Met Ser Gly Pro Thr Gln Ala Pro Gln			
	740	745		750
Gln Pro Pro Met Met	Asn Pro Gln Gln Phe Pro Pro Gly Gln Gln Gln			
	755	760		765
Ala Ala Ile Asn Met	Ala Ala Ile Arg Pro Val Thr Ala Gln Asp Ile			
	770	775		780
Gln Ala Ala Arg Gln	Arg His Pro Ala Met Ala Gln Asn Phe Thr Asp			
785	790	795		800
Asp Gln Ile Arg Glu	Ser Leu Asn Lys Ala Arg Gln Arg Gln Leu Met			
	805	810		815
Leu Leu Ala Gln Gln	Arg Ala Ala Gln Ala Gln Glu Leu Ala Ala Gln			
	820	825		830
Gln Gln Gln Thr Gln	Ala Leu Gln Gln Thr Pro Val Gly Gly Pro Ala			
	835	840		845
Pro Gly Pro His Leu	Arg Pro Glu Gly Pro Gly Gln Pro Ala Thr Gln			
	850	855		860
Pro Gln Gln Gln Ser	Pro Ala Thr Lys Ala Pro Ser Thr Val Pro Gly			
865	870	875		880
Lys Lys Ala Pro Pro	Ala Lys Gln Gln Pro Ala Lys Arg Lys Leu Pro			
	885	890		895
Ser Asp Glu Thr Ala	Asp Ala Gln Asn Pro Asp Asn Gln Val Ala Gln			
	900	905		910

Lys Pro Thr Gln Ala Gly Ala Pro Gln Gly Val Ala Ala Pro Ala Pro  
 915 920 925  
 Ser Lys Pro Asn Met Pro Phe Thr Arg Glu Gln Leu Ala Ala Met Thr  
 930 935 940  
 Pro Gln Gln Arg Ala Gln Ile Glu Ala His Met Arg Arg Gln Gln Gly  
 945 950 955 960  
 Gln Thr Arg Thr Lys Ala Ala Ala Glu Glu Ala Trp Asn Asn Leu Pro  
 965 970 975  
 Glu Lys Ile Arg Gln Ala Tyr His Asp Thr Leu Lys Gln Ala Pro Pro  
 980 985 990  
 Met Lys Phe Ala Ala Ile Thr Pro Glu Gln His Ala Ala Met Asn Gln  
 995 1000 1005  
 Gln Leu Arg Asp Cys Thr Asp Met Leu Gly Arg Met Asp Thr Leu Val  
 1010 1015 1020  
 Gln Trp Phe Ala Lys Ile Pro Gly Gln Glu Lys Asn Val Arg Ser Leu  
 1025 1030 1035 1040  
 Leu Ala Met Arg Ile Gln Leu Met Arg Gln Phe Lys Asn Ser Pro Asp  
 1045 1050 1055  
 Trp Val Leu Asn Asp Ser Leu Thr Ile Ser Pro Glu Asn Leu Thr Ala  
 1060 1065 1070  
 Thr Ile Asn Tyr Ile Lys Lys Leu Phe His Ala Met Ile Thr Arg Val  
 1075 1080 1085  
 Ser Gln His Gln Asn Gln Ala Pro Gly Gln Arg Pro Gly Gly Pro Gln  
 1090 1095 1100  
 Pro Pro Leu Thr Gln Ala Ser Gln Asn Ala Met Pro Ala Leu Asn Ala  
 1105 1110 1115 1120  
 Thr Asn Leu Gln Gln Leu Gln Gln Gln Glu Glu Ala Leu Gln Arg Ala  
 1125 1130 1135  
 Arg Arg Ala Ser Ser Gln Thr Ala Val Ser Ala Thr Ser Ala Val Pro  
 1140 1145 1150  
 Pro Ala Pro Phe Gly Ala Pro Ser Pro Gln Gly Val Pro His Ala Tyr  
 1155 1160 1165  
 Gly Pro Gly Ser Met Pro Pro Glu Gln Leu Lys Leu Pro Pro Pro Lys  
 1170 1175 1180  
 Lys Arg Lys Gln Ser His Pro Gly Ala Thr Pro Thr Val Gly Thr Pro  
 1185 1190 1195 1200  
 Ala Thr Lys Pro Pro Thr Thr Arg Pro Ala Asp Val Lys Met Pro Ala  
 1205 1210 1215  
 Ala Ala Ser Ser His Val Ile Ser Tyr Val Thr Leu Thr Phe Thr Pro  
 1220 1225 1230  
 Ser Ser His Ile Arg Ser Asn Arg Lys Gly Arg Ser  
 1235 1240

&lt;210&gt; 111

&lt;211&gt; 1302

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 111

atgcaaagcc cccagcagcc acccgacttt ctactgtacc cgactcagtc cacgcgtggg 60  
 agcaaaatga tcgccttgga ttcggtccgc cagcagcaga cccattctt ccagaatttc 120  
 accatggatc ctgcattcac ggaccctttc gcattccagg tggacacctt cgctagcttc 180  
 ggacagcccg ccagttcctc tcgaggcccc cagacttcat attatgatac ccctccgctc 240

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tacacggatt cttactccga ctccaataag accgcccctg ggtttccttc catgccgggt 300
acgcccccca cgttccctc caccagccg ctggactccc acgttccggg cctgaccgcc 360
ccgtcgggtc cgtctgtcg cagcgctcc tctcggcca ttgggtcgcc gtactccggc 420
acggcccatg ccaaccagga gaactgggtc gatacgaacc acggcctggg ccttcccgcc 480
gcggtgatgg gggatctgtt tccgaacgac tacacgggga cgacctgga ccccgattac 540
tttgccaata aaggcgcgga cagctttgtt gaccttctt tgatcccgct tcagcagcag 600
tcgaatctgt cgaccccggc catctcctac ccggaacaga ctgattatag cctgggtccc 660
ggcggattct tccctcagtc cctgaccct tcccaattcc aatttgcgga cccctatgg 720
ccattcacac agcagccatg ccccatgccc gcctcatccc catctctgat gccctcccat 780
gtcccgcccc gtctctctc cctctacgac cgtcggctct cgttctcttc cgtgcagtcc 840
cgtcgtctgc agctgagccc ggcgccagc aacgcccaga tcgaggagga cgccaaggaa 900
aagggccgat gccctcatcc ggattgcgg cagctcttcc gggacctgaa agcgcacatg 960
ctgaccgcatc agtcggagcg tccggagaaa tgccccattg tcacttgaga gtaccacacc 1020
aaggggtttg cccgcaagta cgacaagaac cgccacaccc tgaccacta caagggaacg 1080
atggtttgcg gcttctgccc gggatccggg tcgcggccg agaagagctt caaccgggcg 1140
gatgtgttca aacgtcatct gacctctgtg caggtgtgg aacagacccc tcccaactgc 1200
cggaagagaa gcccgcggc cgctcgagt catgtaatta gttatgtcac gcttacattc 1260
acgcccctct cccacatccg ctctaaccga aaaggaagga gt 1302

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<210> 112

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 112

```

Met Gln Ser Pro Gln Gln Pro Pro Asp Phe Leu Leu Tyr Pro Thr Gln
 1          5          10          15
Ser Thr Arg Gly Ser Lys Met Ile Ala Leu Asp Ser Ser Arg Gln Gln
          20          25          30
Gln Thr Pro Phe Phe Gln Asn Phe Thr Met Asp Pro Ala Phe Thr Asp
          35          40          45
Pro Phe Ala Phe Gln Val Asp Thr Phe Ala Ser Phe Gly Gln Pro Ala
          50          55          60
Ser Ser Ser Arg Gly Pro Gln Thr Ser Tyr Tyr Asp Thr Pro Pro Leu
65          70          75          80
Tyr Thr Asp Ser Tyr Ser Asp Ser Asn Lys Thr Ala Pro Gly Phe Pro
          85          90          95
Ser Met Pro Gly Thr Pro Pro Thr Leu Pro Ser Thr Gln Pro Leu Asp
          100          105          110
Ser His Val Pro Gly Leu Thr Ala Pro Ser Gly Pro Ser Val Ala Ser
          115          120          125
Ala Ser Ser Ser Ala Ile Gly Ser Pro Tyr Ser Gly Thr Ala His Ala
          130          135          140
Asn Gln Glu Asn Trp Val Asp Thr Asn His Gly Leu Gly Leu Pro Ala
145          150          155          160
Ala Val Met Gly Asp Leu Phe Pro Asn Asp Tyr Thr Gly Thr Thr Leu
          165          170          175
Asp Pro Asp Tyr Phe Ala Asn Lys Gly Ala Asp Ser Phe Val Asp Pro
          180          185          190
Ser Leu Ile Pro Leu Gln Gln Gln Ser Asn Leu Ser Thr Pro Ala Ile
          195          200          205
Ser Tyr Pro Glu Gln Thr Asp Tyr Ser Leu Val Pro Gly Gly Phe Phe
          210          215          220
Pro Gln Ser Pro Asp Pro Ser Gln Phe Gln Phe Ala Asp Pro Tyr Gly

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225          230          235          240
Pro Phe Thr Gln Gln Pro Cys Pro Met Pro Ala Ser Ser Pro Ser Leu
          245          250          255
Met Pro Ser His Val Pro Pro Arg Arg Leu Ser Leu Tyr Asp Arg Arg
          260          265          270
Ser Ser Val Ser Ser Val Gln Ser Arg Arg Ser Gln Leu Ser Pro Ala
          275          280          285
Ala Ser Asn Ala Glu Ile Glu Glu Asp Ala Lys Glu Lys Gly Arg Cys
          290          295          300
Pro His Pro Asp Cys Gly Arg Val Phe Arg Asp Leu Lys Ala His Met
305          310          315          320
Leu Thr His Gln Ser Glu Arg Pro Glu Lys Cys Pro Ile Val Thr Cys
          325          330          335
Glu Tyr His Thr Lys Gly Phe Ala Arg Lys Tyr Asp Lys Asn Arg His
          340          345          350
Thr Leu Thr His Tyr Lys Gly Thr Met Val Cys Gly Phe Cys Pro Gly
          355          360          365
Ser Gly Ser Pro Ala Glu Lys Ser Phe Asn Arg Ala Asp Val Phe Lys
          370          375          380
Arg His Leu Thr Ser Val His Gly Val Glu Gln Thr Pro Pro Asn Cys
385          390          395          400
Arg Lys Arg Ser Pro Ala Ala Ala Ser Ser His Val Ile Ser Tyr Val
          405          410          415
Thr Leu Thr Phe Thr Pro Ser Ser His Ile Arg Ser Asn Arg Lys Gly
          420          425          430
Arg Ser

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&lt;210&gt; 113

&lt;211&gt; 1071

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 113

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atgctcgagt tagtcgatgc tattccgctt cagacccagc cagttcctcc tgctcctgaa 60
gttcagggttc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
gatttgaacc ttctttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180
ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gcccgcgctt 240
tctcatatac cagaaagagg gatcactgat aactatggtg ttgagccttc gattctagac 300
cttacagatt taggtgatcc ggttcaggac tttaccgtct tcctagaaaag cgtcgggtctc 360
tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaaactagc 420
ctaccatgga actcgaaacc cccagcccgt gagagttcca ggctgggcat cgatacaagt 480
ttgtacaaaa aagcaggctc cacaatgacg gagaaccaca ccccttctac tacgcagccg 540
acgttgctcg cgctgtttgc tgaagccgcg ccgatccaag caaaccgggc tccttctgcc 600
tcagtcacgg cgactgctgc cgccgctact gcggcggtga acaacgcccc ctctatgaac 660
ggcgccggtg agcagttgcc ttgccagtg gttggttgca cggagaagtc ccccaactgcc 720
gagtccttat atgagcatgt ttgcgagcgt catgttgga gtaaaagcac caacaacctc 780
aacctgacct gccagtggg cacttgcaac accacaacag tcaagcgtga tcatatcacc 840
tcccacatcc ggcctcatgt gccacttaag ccgcacaaat ggcacttttg tggtaaggct 900
ttcaagcgcc cccaggattt gaagaagcat gtcaagactc atgcggacga ctccgagatc 960
cgctcccccg aaccgggcat gaagcacctt gatatgatgt tcccccaaaa ccctaagggt 1020
tacgctgctg ccacacatta cttcgaaagc cctatcaacg gcataaatgg g 1071

```



<210> 114  
 <211> 1035  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 114  
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 gttcagggttc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120  
 gatttgaacc ttcttttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180  
 ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgcgcgc gccgcgcgtt 240  
 tctcatatac cagaaagagg gatcactgat aactatggtg ttgagccttc gattctagac 300  
 cttacagatt taggtgatcc ggttcaggac tttaccgtct tcctagaaaag cgtcgggtctc 360  
 tcttcggact gggactccgg catcttctct agttagaag agcccttatt gccaaactagc 420  
 ctacccatgg actcgaaacc cccagcccgt gagagttcca ggctgggcat gacggagaac 480  
 cacacccctt ctactacgca gccgacgttg cctgcgcctg ttgctgaagc cgcgccgac 540  
 caagcaaac ccgctccttc tgcctcagtc acggcgactg ctgccgcgc tactgcggcg 600  
 gtgaacaacg cccctctat gaacggcgcc ggtgagcagt tgccttgcca gtgggttggt 660  
 tgcaacgaga agtccccac tgccgagtct ctatatgagc atgtttgcga gcgtcatgtt 720  
 ggacgtaaaa gcaccaacaa cctcaacctg acctgccagt ggggcacttg caacaccaca 780  
 acagtcaagc gtgatcatat cactccac atccgcgttc atgtgccact taagccgcac 840  
 aaatgcgact tttgtggtaa ggctttcaag cgccccagg atttgaagaa gcatgtcaag 900  
 actcatgagg acgactccga gatccgctcc cccgaaccgg gcatgaagca ccctgatatg 960  
 atgttcccc aaaaccctaa gggttacgt gctgccacac attacttcga aagccctatc 1020  
 aacggcatca atggg 1035

<210> 115  
 <211> 357  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 115  
 Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro  
 1 5 10 15  
 Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala  
 20 25 30  
 His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala  
 35 40 45  
 Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu  
 50 55 60  
 Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Leu  
 65 70 75 80  
 Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro  
 85 90 95  
 Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr  
 100 105 110  
 Val Phe Leu Glu Ser Val Gly Leu Ser Ser Asp Trp Asp Ser Gly Ile  
 115 120 125  
 Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp  
 130 135 140  
 Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Ile Asp Thr Ser  
 145 150 155 160

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Leu Tyr Lys Lys Ala Gly Ser Thr Met Thr Glu Asn His Thr Pro Ser
      165      170      175
Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu Ala Ala Pro Ile
      180      185      190
Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala Thr Ala Ala Ala
      195      200      205
Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn Gly Ala Gly Glu
      210      215      220
Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys Ser Pro Thr Ala
225      230      235      240
Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val Gly Arg Lys Ser
      245      250      255
Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr Cys Asn Thr Thr
      260      265      270
Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg Val His Val Pro
      275      280      285
Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala Phe Lys Arg Pro
290      295      300
Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp Asp Ser Glu Ile
305      310      315      320
Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met Met Phe Pro Gln
      325      330      335
Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe Glu Ser Pro Ile
      340      345      350
Asn Gly Ile Asn Gly
      355

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&lt;210&gt; 116

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 116

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Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
  1      5      10      15
Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
      20      25      30
His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
      35      40      45
Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
      50      55      60
Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Pro Leu
65      70      75      80
Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
      85      90      95
Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
      100      105      110
Val Phe Leu Glu Ser Val Gly Leu Ser Ser Asp Trp Asp Ser Gly Ile
      115      120      125
Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
      130      135      140
Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Met Thr Glu Asn
145      150      155      160

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His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu
      165      170      175
Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala
      180      185      190
Thr Ala Ala Ala Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn
      195      200      205
Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys
      210      215      220
Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val
      225      230      235      240
Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr
      245      250      255
Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg
      260      265      270
Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala
      275      280      285
Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp
      290      295      300
Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met
      305      310      315      320
Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe
      325      330      335
Glu Ser Pro Ile Asn Gly Ile Asn Gly
      340      345

```

&lt;210&gt; 117

&lt;211&gt; 1833

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 117

```

atgaccgccc ccattaccga cgctcagcctg ggggacgagc tccacttaga cggcgaggac 60
gtggcgatgg cgcattgccga cgcgctagac gatttcgatc tggacatggt gggggacggg 120
gattccccgg gtccgggatt tccccccac gactccgccc cctacggcgc tctggatatg 180
gccgacttcg agtttgagca gatgtttacc gatgccctgg gcattgacga ctttggggga 240
atcgatacaa gtttgtacaa aaaagcaggc tccacaatgg atcctagaaa ccatccctct 300
cggcctccgt ctaccagtct gcctcaagga tcggcgccctc ttccttctgc tcccatctcg 360
agcatgccaa tgcctcagta cacgatgcag cctcagtacc cagtctctca gccgcacacc 420
ctgcctcctc tgcaacccca tcatagccag tcgcccgcctc ctactcgtg catggggcag 480
ccgccgtacc ggctgatct gaacaggtag cccgcaccaa gtcacgatgt ttacgcgtct 540
tctgctgcgc cgataatgcc ccacactacc gtgggcagct tgcctccgac atctttcctt 600
tctcatccca atccgcaggc gcaggcacag gcgcagcaat cgcgcgacta tcctcctcct 660
catagcgtgc tccgcgccgc ttccagcgct cagtcgtacc cgcagccaat tgcgcggcgg 720
cctccccggg accgtcgtgc tgacttcaac aatggacttc cttcaggagc attcagttat 780
tcggacggaa agcctcaagg ttgggacccc gttgctgcga atggtgctgc gccgtatccc 840
gggaaggact cccccgaac ccagggtgtt ggttctcagg ggcgacgcgg tatecttccg 900
agtgttccgg gacgcgcaac tccggtcaca aatggtgtta acggcaccgg caagaacact 960
actatccccg ccaaggatgc cgatggaaag ttcccttgcc cgaactgtaa caagacttat 1020
cttcatgcca agcatctcaa gcgccatctg ctacgccaca ctggtgaccg cccgtacatg 1080
tgtgttcttt gcaaagacac cttctctcgc agtgatatcc tgaaacgtca tttccaaaaa 1140
tgctcaatca ggcgtggtaa ccccaaccga gcaacgcact tgtcgcaccc caatgcgcat 1200
gtgaagaggt cccaacagca ggctgcggcg aatcctgtaa aacctgtcca ggatgaagtc 1260
agtagtaccg tccgcctcc caatggcatc ccgggcacga cttacggcga gggagccgtc 1320

```

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aacggcaatg gactagctcc ggccccggcca gggtagcgcg atcaccagac tatgggcttc 1380
ccaatgtcat ccgtcaacgg gatgggccgt ggtcagcctg aagacgcgtt tccccgggc 1440
cggccgcacg aaggagcccc ttggccacaa gctcccaagc agagcccgta tctcgtgcag 1500
ccgggtgctg acccttctgg ccaccagttg aatattgacc gaaacatcga gcaggtaaaa 1560
caaccggttg ttcaagaccc caagcgccct gtgatgccag gacatcccgg ccaccccggt 1620
gagcttgact ggacgtctat gttccaacct caagctcccg agggctacat gttctcccag 1680
tctatgcctg gtggtcaaga gcccatccac gctcatgtcg agaccgagcg aaagtattac 1740
cccaccacta ccgctggtca agagagtgga atgaacggtc tctatctggc ttcgactatg 1800
agtggcgacg gcaccgttca gcccggcaga caa

```

<210> 118

<211> 1800

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 118

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gtggcgatgg cgcagtcgga cgcgctagac gatttcgacg tggacatgtt gggggacggg 120
gattccccgg gtccgggatt tccccccac gactccgccc cctacggcgc tctggatatg 180
gccgacttcg agttttagca gatgtttacc gatgccctgg gcattgacga ctttggggga 240
atcatggatc ctagaaacca tcctctcggg cctccgtcta ccagtctgcc tcaaggatcg 300
gcgcctcttc cttctgctcc catctcgagc atgccaatgc ctacgtacac gatgcagcct 360
cagtaccagc tctctcagcc gcacaccctg cctcctctgc aaccccatca tagccagtcg 420
cccgctcctc actcgtacat ggggcagccg ccgtaccggc ctgatctgaa caggtacccc 480
gcatcaagtc acgatgttta cgcgtcttct gctgcgcgga taatgcccc cactaccgtg 540
ggcagcttgc ctccgacatc ttctcttctt catcccaatc cgcaggcgca ggcacaggcg 600
cagcaatcgc cgcactatcc tcctcctcat agcgtgctcc cgcccgcttc cagcgctcag 660
tcgtaccgca agccaattgc gccggcgccg ccccgggacc gtcgtgctga cttcaacaat 720
ggacttcctt caggagcatt cagttattcg gacggaaagc ctcaagggtg ggaccccggt 780
gctgcgaatg gtgctgcgcc gtatcccggg aaggactccc cccgaacca gggtgttgtg 840
tctcaggggc gacgcggtat ccttccgagt gttccgggac gcgcaactcc ggtcacaaat 900
ggtgttaacg gcaccggcaa gaacactact atcccgccca aggatgccga tggaaagtgc 960
ccttgccgca actgtaacaa gacttatctt catgccaagc atctcaagcg ccattctgcta 1020
cgccacactg gtgaccgccc gtacatgtgt gttcttttgc aagacacctt ctctcgagc 1080
gatatcctga aacgtcattt ccaaaaatgc tcaatcaggc gtggttaacc caccggagca 1140
acgcacttgt cgcaccccaa tgcgcatgtg aagaggtccc aacagcaggc tgcggcgaat 1200
cctgtaaaac ctgtccagga tgaagtcagt agtacgctcc cgcctcccaa tggcatcccg 1260
ggcacgactt acggcgaggg agccgtcaac ggcaatggac tagctccggc ccggccaggg 1320
tacgcggatc accagactat gggcttccca atgtcatccg tcaacgggat gggccgtggt 1380
cagcctgaag acgcgtttcc cggcgggcgg ccgcatcaag gagccccttg gccacaagct 1440
cccaagcaga gcccgtatct cgtgcagccg ggtgctgacc cttctggcca ccagttgaat 1500
attgaccgaa acatcgagca ggtaaaacaa ccggtgtgtc aagaccccaa gcgcctgtg 1560
atgccaggac atcccgcca ccccggtgag cttgactgga cgtctatgtt ccaacctcaa 1620
gtcctcgagg gctacatgtt ctcccagctc atgcctggtg gtcaagagcc catccacgct 1680
catgtcgaga ccgagcgaaa gtattacccc accactaccg ctggtcaaga gagtggaaatg 1740
aacggtctct atctggcttc gactatgagt ggcgacggca ccgttcagcc cgccagacaa 1800

```

<210> 119

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

&lt;223&gt; fungal gene

&lt;400&gt; 119

```

Met Thr Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
 1          5          10          15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
          20          25          30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
          35          40          45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
          50          55          60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
65          70          75          80
Ile Asp Thr Ser Leu Tyr Lys Lys Ala Gly Ser Thr Met Asp Pro Arg
          85          90          95
Asn His Pro Ser Arg Pro Pro Ser Thr Ser Leu Pro Gln Gly Ser Ala
          100          105          110
Pro Leu Pro Ser Ala Pro Ile Ser Ser Met Pro Met Pro Gln Tyr Thr
          115          120          125
Met Gln Pro Gln Tyr Pro Val Ser Gln Pro His Thr Leu Pro Pro Leu
          130          135          140
Gln Pro His His Ser Gln Ser Pro Ala Pro His Ser Tyr Met Gly Gln
145          150          155          160
Pro Pro Tyr Arg Pro Asp Leu Asn Arg Tyr Pro Ala Ser Ser His Asp
          165          170          175
Val Tyr Ala Ser Ser Ala Ala Pro Ile Met Pro His Thr Thr Val Gly
          180          185          190
Ser Leu Pro Pro Thr Ser Phe Leu Ser His Pro Asn Pro Gln Ala Gln
          195          200          205
Ala Gln Ala Gln Gln Ser Pro His Tyr Pro Pro Pro His Ser Val Leu
          210          215          220
Pro Pro Ala Ser Ser Ala Gln Ser Tyr Pro Gln Pro Ile Ala Pro Ala
225          230          235          240
Pro Pro Arg Asp Arg Arg Ala Asp Phe Asn Asn Gly Leu Pro Ser Gly
          245          250          255
Ala Phe Ser Tyr Ser Asp Gly Lys Pro Gln Gly Trp Asp Pro Val Ala
          260          265          270
Ala Asn Gly Ala Ala Pro Tyr Pro Gly Lys Asp Ser Pro Arg Thr Gln
          275          280          285
Val Val Gly Ser Gln Gly Arg Arg Gly Ile Leu Pro Ser Val Pro Gly
          290          295          300
Arg Ala Thr Pro Val Thr Asn Gly Val Asn Gly Thr Gly Lys Asn Thr
305          310          315          320
Thr Ile Pro Ala Lys Asp Ala Asp Gly Lys Phe Pro Cys Pro Asn Cys
          325          330          335
Asn Lys Thr Tyr Leu His Ala Lys His Leu Lys Arg His Leu Leu Arg
          340          345          350
His Thr Gly Asp Arg Pro Tyr Met Cys Val Leu Cys Lys Asp Thr Phe
          355          360          365
Ser Arg Ser Asp Ile Leu Lys Arg His Phe Gln Lys Cys Ser Ile Arg
          370          375          380
Arg Gly Asn Pro Thr Gly Ala Thr His Leu Ser His Pro Asn Ala His
385          390          395          400
Val Lys Arg Ser Gln Gln Gln Ala Ala Ala Asn Pro Val Lys Pro Val
          405          410          415
Gln Asp Glu Val Ser Ser Thr Val Pro Pro Pro Asn Gly Ile Pro Gly
          420          425          430

```

```

Thr Thr Tyr Gly Glu Gly Ala Val Asn Gly Asn Gly Leu Ala Pro Ala
    435                      440                      445
Arg Pro Gly Tyr Ala Asp His Gln Thr Met Gly Phe Pro Met Ser Ser
    450                      455                      460
Val Asn Gly Met Gly Arg Gly Gln Pro Glu Asp Ala Phe Pro Gly Gly
    465                      470                      475                      480
Arg Pro His Gln Gly Ala Pro Trp Pro Gln Ala Pro Lys Gln Ser Pro
    485                      490                      495
Tyr Leu Val Gln Pro Gly Ala Asp Pro Ser Gly His Gln Leu Asn Ile
    500                      505                      510
Asp Arg Asn Ile Glu Gln Val Lys Gln Pro Val Val Gln Asp Pro Lys
    515                      520                      525
Arg Pro Val Met Pro Gly His Pro Gly His Pro Gly Glu Leu Asp Trp
    530                      535                      540
Thr Ser Met Phe Gln Pro Gln Ala Pro Glu Gly Tyr Met Phe Ser Gln
    545                      550                      555                      560
Ser Met Pro Gly Gly Gln Glu Pro Ile His Ala His Val Glu Thr Glu
    565                      570                      575
Arg Lys Tyr Tyr Pro Thr Thr Thr Ala Gly Gln Glu Ser Gly Met Asn
    580                      585                      590
Gly Leu Tyr Leu Ala Ser Thr Met Ser Gly Asp Gly Thr Val Gln Pro
    595                      600                      605
Ala Arg Gln
    610

```

&lt;210&gt; 120

&lt;211&gt; 600

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 120

```

Met Thr Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
  1      5      10      15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
    20      25      30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
    35      40      45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
    50      55      60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
    65      70      75      80
Ile Met Asp Pro Arg Asn His Pro Ser Arg Pro Pro Ser Thr Ser Leu
    85      90      95
Pro Gln Gly Ser Ala Pro Leu Pro Ser Ala Pro Ile Ser Ser Met Pro
    100     105     110
Met Pro Gln Tyr Thr Met Gln Pro Gln Tyr Pro Val Ser Gln Pro His
    115     120     125
Thr Leu Pro Pro Leu Gln Pro His His Ser Gln Ser Pro Ala Pro His
    130     135     140
Ser Tyr Met Gly Gln Pro Pro Tyr Arg Pro Asp Leu Asn Arg Tyr Pro
    145     150     155     160
Ala Ser Ser His Asp Val Tyr Ala Ser Ser Ala Ala Pro Ile Met Pro
    165     170     175

```

```

His Thr Thr Val Gly Ser Leu Pro Pro Thr Ser Phe Leu Ser His Pro
      180                      185                      190
Asn Pro Gln Ala Gln Ala Gln Ala Gln Gln Ser Pro His Tyr Pro Pro
      195                      200                      205
Pro His Ser Val Leu Pro Pro Ala Ser Ser Ala Gln Ser Tyr Pro Gln
      210                      215                      220
Pro Ile Ala Pro Ala Pro Pro Arg Asp Arg Arg Ala Asp Phe Asn Asn
      225                      230                      235                      240
Gly Leu Pro Ser Gly Ala Phe Ser Tyr Ser Asp Gly Lys Pro Gln Gly
      245                      250                      255
Trp Asp Pro Val Ala Ala Asn Gly Ala Ala Pro Tyr Pro Gly Lys Asp
      260                      265                      270
Ser Pro Arg Thr Gln Val Val Gly Ser Gln Gly Arg Arg Gly Ile Leu
      275                      280                      285
Pro Ser Val Pro Gly Arg Ala Thr Pro Val Thr Asn Gly Val Asn Gly
      290                      295                      300
Thr Gly Lys Asn Thr Thr Ile Pro Ala Lys Asp Ala Asp Gly Lys Phe
      305                      310                      315                      320
Pro Cys Pro Asn Cys Asn Lys Thr Tyr Leu His Ala Lys His Leu Lys
      325                      330                      335
Arg His Leu Leu Arg His Thr Gly Asp Arg Pro Tyr Met Cys Val Leu
      340                      345                      350
Cys Lys Asp Thr Phe Ser Arg Ser Asp Ile Leu Lys Arg His Phe Gln
      355                      360                      365
Lys Cys Ser Ile Arg Arg Gly Asn Pro Thr Gly Ala Thr His Leu Ser
      370                      375                      380
His Pro Asn Ala His Val Lys Arg Ser Gln Gln Gln Ala Ala Ala Asn
      385                      390                      395                      400
Pro Val Lys Pro Val Gln Asp Glu Val Ser Ser Thr Val Pro Pro Pro
      405                      410                      415
Asn Gly Ile Pro Gly Thr Thr Tyr Gly Glu Gly Ala Val Asn Gly Asn
      420                      425                      430
Gly Leu Ala Pro Ala Arg Pro Gly Tyr Ala Asp His Gln Thr Met Gly
      435                      440                      445
Phe Pro Met Ser Ser Val Asn Gly Met Gly Arg Gly Gln Pro Glu Asp
      450                      455                      460
Ala Phe Pro Gly Gly Arg Pro His Gln Gly Ala Pro Trp Pro Gln Ala
      465                      470                      475                      480
Pro Lys Gln Ser Pro Tyr Leu Val Gln Pro Gly Ala Asp Pro Ser Gly
      485                      490                      495
His Gln Leu Asn Ile Asp Arg Asn Ile Glu Gln Val Lys Gln Pro Val
      500                      505                      510
Val Gln Asp Pro Lys Arg Pro Val Met Pro Gly His Pro Gly His Pro
      515                      520                      525
Gly Glu Leu Asp Trp Thr Ser Met Phe Gln Pro Gln Ala Pro Glu Gly
      530                      535                      540
Tyr Met Phe Ser Gln Ser Met Pro Gly Gly Gln Glu Pro Ile His Ala
      545                      550                      555                      560
His Val Glu Thr Glu Arg Lys Tyr Tyr Pro Thr Thr Thr Ala Gly Gln
      565                      570                      575
Glu Ser Gly Met Asn Gly Leu Tyr Leu Ala Ser Thr Met Ser Gly Asp
      580                      585                      590
Gly Thr Val Gln Pro Ala Arg Gln
      595                      600

```

&lt;210&gt; 121

&lt;211&gt; 1353

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 121

```

atgaccgccc ccattaccga cgtcagcctg ggggacgagc tccacttaga cggcgaggac 60
gtggcgatgg cgcattgccga cgcgctagac gatttcgacg tggacatggt gggggacggg 120
gattccccgg gtccgggatt tccccccac gactccgccc cctacggcgc tctggatatg 180
gccgacttcg agtttgagca gatgtttacc gatgccctgg gcattgacga ctttggggga 240
atcgatacaa gtttgtacaa aaaagcaggc tccacaatgg ttcttctcaa aaagcatttg 300
aaagatgtca accgtgagga tcagaggcaa atgccgaggc aacggctgcc atctattcaa 360
gaaatatttg gggagacttt tctggcgatt ccttcaaate catcatatgc actgccttct 420
cacaccagac atgccgctcc accggctttg ccggctgtgt atgaaattgc ccattcaatc 480
gaaggggctc cgtcaaataga gcaagggtta ttacccaaaa ttcaacagt ggagagatct 540
ttgggcatta tctctcccg tcaatgagctc cagcatccgg aggtaatacg cccggaaaaa 600
ccatccttct ctccgaacgg ttgttctctt aacgaaagcc gtcgcttttc aaagcacccg 660
gacatatcta tacctcaacc ggggtttattg tcatgcgac ccatggattt agcacagccg 720
tcctttgtcg aacctccaaa tgtgtttcat ggatttccca tcaggaaaat accaaactcg 780
ataccgcctc agccaaagca gttatgtctg ccggaaaaac gaacaccgag ttctcttgat 840
ttcagtctgt tttttaaggt gatcgagaca gtcagcgcac agacctggc tttcgtgctg 900
tatcactccg caatgagtca gtcagacaac catcaaagat ccctccctgg actatctatc 960
actgagataa atggcctcct cagtcaggag cagcaaaagc aggatgtctt gatttatatt 1020
agggatgaac ttgtgcgctt cgaccaatac caagccttag cgcagcagaa tactcgggca 1080
gccgcatgta tggcgggtgg ggctgaccga ggtctttgtt catcagtcac taaacagagc 1140
aagacccata aagtctctaa acaaaaaaga gaatggcacg gggatagtgc tcttcgttgt 1200
catagctgca accgttctga aacaccagaa tggcgtcgtg gtccggacgg cccccgaact 1260
ctttgtaacg cctgtggttt acattatgca aaattgtctc gacgaacggg caaatttgtg 1320
gcgttggacg atattggcat caggggcaaa aca
1353

```

&lt;210&gt; 122

&lt;211&gt; 1320

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 122

```

atgaccgccc ccattaccga cgtcagcctg ggggacgagc tccacttaga cggcgaggac 60
gtggcgatgg cgcattgccga cgcgctagac gatttcgacg tggacatggt gggggacggg 120
gattccccgg gtccgggatt tccccccac gactccgccc cctacggcgc tctggatatg 180
gccgacttcg agtttgagca gatgtttacc gatgccctgg gcattgacga ctttggggga 240
atcatggttc ttctcaaaaa gcatttgaaa gatgtcaacc gtgaggatca gaggcaaatg 300
ccgaggcaac ggctgccatc tattcaagaa atatttgggg agacttttct ggcgattcct 360
tcaaataccat catatgcact gccttctcac accagacatg ccgctccacc ggctttgccg 420
gctgtgtatg aaattgccca ttcaatcgaa ggggctccgt caaatgagca aggtttatta 480
cccaaaatth caacagtgga gagatctttg ggcattatct ctcccgtaa tgagctccag 540
catccggagg taatacgccc ggaaaatcca tccttctctc cgaacggttg ttctcttaac 600
gaaagccgtc gcttttcaaa gcacccggac ctatctatac ctcaaccggg tttattgtca 660
tgcgatccca tggatttagc acagccgtcc ttgtcgaa ctcctcaatgt gtttcatgga 720
tttcccatca ggaaaatacc aaactcgata ccgcctcagc caaagcagtt atgtctgccg 780
gaaaaacgaa caccgagttc tcttgatttc agtctgtttt ttaaggtgat cgagacagtc 840
agcgacagca ccttggtttt cgtgcggtat cactccgcaa tgagtcagtc agacaaccat 900
caaagatccc tccctggact atctatcact gagataaatg gcctcctcag tcaggagcag 960

```



```

caaaagcagg atgtcttgat ttatattagg gatgaacttg tgcgcttcga ccaataccaa 1020
gccttagcgc agcagaatac tcgggcagcc gcatgtatgg cgggtggggc tgaccgaggt 1080
ctttgttcat cagtcactaa acagagcaag acccataaag tctctaaaca aaaaagagaa 1140
tggcacgggg atagtgtctt tcgttgtcat agctgcaacc gttctgaaac accagaatgg 1200
cgctgtgggc cggacggccc ccgaactctt tgtaacgcct gtgggtttaca ttatgcaaaa 1260
ttgtctcgac gaacgggcaa atttgtggcg ttggacgata ttggcatcag gggcaaaaaca 1320

```

<210> 123

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 123

```

Met Thr Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
 1           5           10           15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
      20           25           30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
      35           40           45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
 50           55           60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
65           70           75           80
Ile Asp Thr Ser Leu Tyr Lys Lys Ala Gly Ser Thr Met Val Leu Leu
      85           90           95
Lys Lys His Leu Lys Asp Val Asn Arg Glu Asp Gln Arg Gln Met Pro
      100          105          110
Arg Gln Arg Leu Pro Ser Ile Gln Glu Ile Phe Gly Glu Thr Phe Leu
      115          120          125
Ala Ile Pro Ser Asn Pro Ser Tyr Ala Leu Pro Ser His Thr Arg His
130          135          140
Ala Ala Pro Pro Ala Leu Pro Ala Val Tyr Glu Ile Ala His Ser Ile
145          150          155          160
Glu Gly Ala Pro Ser Asn Glu Gln Gly Leu Leu Pro Lys Ile Ser Thr
      165          170          175
Val Glu Arg Ser Leu Gly Ile Ile Ser Pro Val Asn Glu Leu Gln His
      180          185          190
Pro Glu Val Ile Arg Pro Glu Asn Pro Ser Phe Ser Pro Asn Gly Cys
      195          200          205
Ser Leu Asn Glu Ser Arg Arg Phe Ser Lys His Pro Asp Leu Ser Ile
210          215          220
Pro Gln Pro Gly Leu Leu Ser Cys Asp Pro Met Asp Leu Ala Gln Pro
225          230          235          240
Ser Phe Val Glu Pro Pro Asn Val Phe His Gly Phe Pro Ile Arg Lys
      245          250          255
Ile Pro Asn Ser Ile Pro Pro Gln Pro Lys Gln Leu Cys Leu Pro Glu
260          265          270
Lys Arg Thr Pro Ser Ser Leu Asp Phe Ser Leu Phe Phe Lys Val Ile
      275          280          285
Glu Thr Val Ser Ala Gln Thr Leu Ala Phe Val Arg Tyr His Ser Ala
290          295          300
Met Ser Gln Ser Asp Asn His Gln Arg Ser Leu Pro Gly Leu Ser Ile
305          310          315          320

```

```

Thr Glu Ile Asn Gly Leu Leu Ser Gln Glu Gln Gln Lys Gln Asp Val
      325      330      335
Leu Ile Tyr Ile Arg Asp Glu Leu Val Arg Phe Asp Gln Tyr Gln Ala
      340      345      350
Leu Ala Gln Gln Asn Thr Arg Ala Ala Ala Cys Met Ala Gly Gly Ala
      355      360      365
Asp Arg Gly Leu Cys Ser Ser Val Thr Lys Gln Ser Lys Thr His Lys
      370      375      380
Val Ser Lys Gln Lys Arg Glu Trp His Gly Asp Ser Ala Leu Arg Cys
      385      390      395      400
His Ser Cys Asn Arg Ser Glu Thr Pro Glu Trp Arg Arg Gly Pro Asp
      405      410      415
Gly Pro Arg Thr Leu Cys Asn Ala Cys Gly Leu His Tyr Ala Lys Leu
      420      425      430
Ser Arg Arg Thr Gly Lys Phe Val Ala Leu Asp Asp Ile Gly Ile Arg
      435      440      445
Gly Lys Thr
      450

```

&lt;210&gt; 124

&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 124

```

Met Thr Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
  1      5      10      15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
      20      25      30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
      35      40      45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
      50      55      60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
      65      70      75      80
Ile Met Val Leu Leu Lys Lys His Leu Lys Asp Val Asn Arg Glu Asp
      85      90      95
Gln Arg Gln Met Pro Arg Gln Arg Leu Pro Ser Ile Gln Glu Ile Phe
      100      105      110
Gly Glu Thr Phe Leu Ala Ile Pro Ser Asn Pro Ser Tyr Ala Leu Pro
      115      120      125
Ser His Thr Arg His Ala Ala Pro Pro Ala Leu Pro Ala Val Tyr Glu
      130      135      140
Ile Ala His Ser Ile Glu Gly Ala Pro Ser Asn Glu Gln Gly Leu Leu
      145      150      155      160
Pro Lys Ile Ser Thr Val Glu Arg Ser Leu Gly Ile Ile Ser Pro Val
      165      170      175
Asn Glu Leu Gln His Pro Glu Val Ile Arg Pro Glu Asn Pro Ser Phe
      180      185      190
Ser Pro Asn Gly Cys Ser Leu Asn Glu Ser Arg Arg Phe Ser Lys His
      195      200      205
Pro Asp Leu Ser Ile Pro Gln Pro Gly Leu Leu Ser Cys Asp Pro Met
      210      215      220

```

Asp	Leu	Ala	Gln	Pro	Ser	Phe	Val	Glu	Pro	Pro	Asn	Val	Phe	His	Gly
225					230					235					240
Phe	Pro	Ile	Arg	Lys	Ile	Pro	Asn	Ser	Ile	Pro	Pro	Gln	Pro	Lys	Gln
				245					250					255	
Leu	Cys	Leu	Pro	Glu	Lys	Arg	Thr	Pro	Ser	Ser	Leu	Asp	Phe	Ser	Leu
			260					265					270		
Phe	Phe	Lys	Val	Ile	Glu	Thr	Val	Ser	Ala	Gln	Thr	Leu	Ala	Phe	Val
		275					280					285			
Arg	Tyr	His	Ser	Ala	Met	Ser	Gln	Ser	Asp	Asn	His	Gln	Arg	Ser	Leu
	290					295					300				
Pro	Gly	Leu	Ser	Ile	Thr	Glu	Ile	Asn	Gly	Leu	Leu	Ser	Gln	Glu	Gln
305					310					315					320
Gln	Lys	Gln	Asp	Val	Leu	Ile	Tyr	Ile	Arg	Asp	Glu	Leu	Val	Arg	Phe
			325						330					335	
Asp	Gln	Tyr	Gln	Ala	Leu	Ala	Gln	Gln	Asn	Thr	Arg	Ala	Ala	Ala	Cys
			340					345					350		
Met	Ala	Gly	Gly	Ala	Asp	Arg	Gly	Leu	Cys	Ser	Ser	Val	Thr	Lys	Gln
	355						360					365			
Ser	Lys	Thr	His	Lys	Val	Ser	Lys	Gln	Lys	Arg	Glu	Trp	His	Gly	Asp
	370					375					380				
Ser	Ala	Leu	Arg	Cys	His	Ser	Cys	Asn	Arg	Ser	Glu	Thr	Pro	Glu	Trp
385					390					395					400
Arg	Arg	Gly	Pro	Asp	Gly	Pro	Arg	Thr	Leu	Cys	Asn	Ala	Cys	Gly	Leu
			405					410						415	
His	Tyr	Ala	Lys	Leu	Ser	Arg	Arg	Thr	Gly	Lys	Phe	Val	Ala	Leu	Asp
			420					425					430		
Asp	Ile	Gly	Ile	Arg	Gly	Lys	Thr								
	435						440								

&lt;210&gt; 125

&lt;211&gt; 1071

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 125

```

atgctcgagt tagtcgatgc tattccgctt cagacccagc cagttcctcc tgctcctgaa 60
gttcagggttc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
gatttgaacc ttcttttctca tgccgcgagt catgtcgtct ttgagggaca acaagaaagt 180
ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gccgccgctt 240
tctcatatac cagaaagagg gatcactgat aactatggtg ttgagccttc gattctagac 300
cttacagatt taggtgatcc gggttcaggac ttaccgtct tccagaaag cgtctgtctc 360
tcttcggact gggactccgg catcttctct agttagaag agcccttatt gccaaactagc 420
ctacccatgg actcgaaacc cccagcccgt gagagttcca ggctgggcat cgatacaagt 480
ttgtacaaaa aagcaggctc cacaatgacg gagaaccaca ccccttctac tacgcagccg 540
acgttgccctg cgctgtgtgc tgaagccgcg ccgatccaag caaaccggc tccttctgcc 600
tcagtcacgg cgactgctgc cgccgtact gcggcgggtga acaacgcccc ctctatgaac 660
ggcgccggtg agcagttgcc ttgccagtg gttggttgca cggagaagtc cccactgcc 720
gagttcttat atgagcatgt ttgcgagcgt catgttgga gtaaaagcac caacaacctc 780
aacctgacct gccagtggg cacttgcaac accacaacag tcaagcgtga tcatatcacc 840
tcccacatcc gcgttcatt gccacttaag ccgcacaaat gcgacttttg tggttaaggct 900
ttcaagcgcc ccaggattt gaagaagcat gtcaagactc atgcggacga ctccgagatc 960
cgctcccccg aaccgggcat gaagcacctc gatatgatgt tcccccaaaa ccctaagggt 1020
tacgtctgctg ccacacatta cttcgaaagc cctatcaacg gcatcaatgg g 1071

```

<210> 126  
 <211> 1035  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 126  
 atgctcgagt tagtcgatgc tattccgctt cagacccagc cagttcctcc tgctcctgaa 60  
 gttcagggtt agccccctcc aatcgtaggag acgccccatt tcaacccttc atggggatat 120  
 gatttgaacc ttcttttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180  
 ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gccgccgctt 240  
 tctcatatac cagaaagagg gatcactgat aactatgggtg ttgagccttc gattctagac 300  
 cttacagatt taggtgatcc gggtcaggac tttaccgtct tcctagaaag cgtctgtctc 360  
 tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaaactagc 420  
 ctacccatgg actcgaaacc cccagcccgt gagagttcca ggctgggcat gacggagaac 480  
 cacaccctt ctactacgca gccgacgttg cctgcgcctg ttgctgaagc cgcgccgac 540  
 caagcaaac cggctccttc tgccctcagtc acggcgactg ctgccgccgc tactgcggcg 600  
 gtgaacaacg cccctctat gaacggcgcc ggtgagcagt tgccttgcca gtgggttggt 660  
 tgacggaga agtccccac tgccgagtct ctatatgagc atgtttgcga gcgtcatgtt 720  
 ggacgtaaaa gcaccaacaa cctcaacctg acctgccagt ggggcacttg caacaccaca 780  
 acagtcaagc gtgatcatat cacctccac atccgcgttc atgtgccact taagccgcac 840  
 aaatgcgact tttgtggtaa ggctttcaag cgcccccagg atttgaagaa gcatgtcaag 900  
 actcatgcgg acgactccga gatccgctcc cccgaaccgg gcatgaagca ccctgatatg 960  
 atgttcccc aaaaccctaa gggttacgct gctgccacac attacttcga aagccctatc 1020  
 aacggcatca atggg 1035

<210> 127  
 <211> 357  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 127  
 Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro  
 1 5 10 15  
 Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala  
 20 25 30  
 His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala  
 35 40 45  
 Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu  
 50 55 60  
 Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Pro Leu  
 65 70 75 80  
 Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro  
 85 90 95  
 Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr  
 100 105 110  
 Val Phe Leu Glu Ser Val Cys Leu Ser Ser Asp Trp Asp Ser Gly Ile  
 115 120 125  
 Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp  
 130 135 140  
 Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Ile Asp Thr Ser

```

145          150          155          160
Leu Tyr Lys Lys Ala Gly Ser Thr Met Thr Glu Asn His Thr Pro Ser
          165          170          175
Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu Ala Ala Pro Ile
          180          185          190
Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala Thr Ala Ala Ala
          195          200          205
Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn Gly Ala Gly Glu
          210          215          220
Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys Ser Pro Thr Ala
225          230          235          240
Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val Gly Arg Lys Ser
          245          250          255
Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr Cys Asn Thr Thr
          260          265          270
Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg Val His Val Pro
          275          280          285
Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala Phe Lys Arg Pro
          290          295          300
Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp Asp Ser Glu Ile
305          310          315          320
Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met Met Phe Pro Gln
          325          330          335
Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe Glu Ser Pro Ile
          340          345          350
Asn Gly Ile Asn Gly
          355

```

&lt;210&gt; 128

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 128

```

Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
 1          5          10          15
Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
          20          25          30
His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
          35          40          45
Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
          50          55          60
Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Leu
65          70          75          80
Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
          85          90          95
Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
          100          105          110
Val Phe Leu Glu Ser Val Cys Leu Ser Ser Asp Trp Asp Ser Gly Ile
          115          120          125
Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
130          135          140
Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Met Thr Glu Asn

```

```

145          150          155          160
His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu
          165          170          175
Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala
          180          185          190
Thr Ala Ala Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn
          195          200          205
Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys
          210          215          220
Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val
225          230          235          240
Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr
          245          250          255
Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg
          260          265          270
Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala
          275          280          285
Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp
          290          295          300
Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met
305          310          315          320
Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe
          325          330          335
Glu Ser Pro Ile Asn Gly Ile Asn Gly
          340          345

```

```

<210> 129
<211> 1071
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> fungal gene

```

```

<400> 129
atgctcgagt tagtcgatgc tattccgctt cagaccagc cagttccctc tgctcctgaa 60
gttcagggtc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
gatttgaacc ttctttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180
ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gccgccgctt 240
tctcatatac cagaaagagg gatcactgat aactatggtg ttgagccttc gattctagac 300
cttacagatt taggtgatcc gggtcaggac ttaccgtct tcctagaaag cgtcgatctc 360
tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaaactagc 420
ctacccatgg actcgaaacc cccagcccgt gagagttcca ggctgggcat cgatacaagt 480
ttgtacaaaa aagcaggctc cacaatgacg gagaaccaca ccccttctac tacgcagccg 540
acgttgctg cgcctgttgc tgaagccgcg ccgatccaag caaacccggc tccttctgcc 600
tcagtcacgg cgactgctgc cgccgtact gcggcggtga acaacgcccc ctctatgaac 660
ggcgccggtg agcagttgcc ttgccagtgg gttggttgca cggagaagtc cccactgcc 720
gagtctctat atgagcatgt ttgcgagcgt catgttggac gtaaaagcac caacaacctc 780
aacctgacat gccagtgggg cacttgcaac accacaacag tcaagcgtga tcatatcacc 840
tcccacatcc gcgttcattg gccacttaag ccgcacaaat gcgacttttg tggttaaggct 900
ttcaagcgcc cccaggattt gaagaagcat gtcaagactc atgcggacga ctccgagatc 960
cgctcccccg aaccgggcat gaagcaccct gatatgatgt tccccaaaaa ccctaagggt 1020
tacgctgctg ccacacatta cttcgaaagc cctatcaacg gcatcaatgg g 1071

```

```

<210> 130
<211> 1035

```

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 130

```

atgctcgagt tagtcgatgc tattccgctt cagacccagc cagttcctcc tgctcctgaa 60
gttcagggttc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
gatttgaacc ttcttttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180
ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gccgccgctt 240
tctcatatac cagaaagagg gatcactgat aactatgggtg ttgagccttc gattctagac 300
cttacagatt taggtgatcc gggttcaggac tttaccgtct tcctagaaag cgtcgatctc 360
tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaactagc 420
ctacccatgg actcgaacc cccagcccgt gagagttcca ggctgggcat gacggagaac 480
cacaccctt ctactacga gccgacgttg cctgcgcctg ttgctgaagc cgcgccgatc 540
caagcaaacc cggctccttc tgcctcagtc acggcgactg ctgccgccgc tactgcggcg 600
gtgaacaacg cccctctat gaacggcgcc ggtgagcagt tgccttgcca gtgggttggt 660
tgacggaga agtccccac tgccgagtct ctatatgagc atgtttgca gcgtcatgtt 720
ggacgtaaaa gcaccaacaa cctcaacctg acctgccagt ggggcacttg caacaccaca 780
acagtcaagc gtgatcatat cacctccac atccgcgttc atgtgccact taagcgcac 840
aaatgcgact tttgtggtaa ggctttcaag cgcgcccagg atttgaagaa gcatgtcaag 900
actcatgcgg acgactccga gatccgctcc cccgaaccgg gcatgaagca cctgatatg 960
atgttcccc aaaaccctaa gggttacgt gctgccacac attacttcga aagccctatc 1020
aacggcatca atggg                                     1035

```

&lt;210&gt; 131

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 131

```

Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
 1          5          10          15
Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
 20          25          30
His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
 35          40          45
Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
 50          55          60
Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Leu
 65          70          75          80
Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
 85          90          95
Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
100          105          110
Val Phe Leu Glu Ser Val Asp Leu Ser Ser Asp Trp Asp Ser Gly Ile
115          120          125
Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
130          135          140
Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Ile Asp Thr Ser
145          150          155          160
Leu Tyr Lys Lys Ala Gly Ser Thr Met Thr Glu Asn His Thr Pro Ser
165          170          175

```

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```

Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu Ala Ala Pro Ile
      180      185      190
Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala Thr Ala Ala Ala
      195      200      205
Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn Gly Ala Gly Glu
      210      215      220
Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys Ser Pro Thr Ala
225      230      235      240
Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val Gly Arg Lys Ser
      245      250      255
Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr Cys Asn Thr Thr
      260      265      270
Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg Val His Val Pro
      275      280      285
Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala Phe Lys Arg Pro
      290      295      300
Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp Asp Ser Glu Ile
305      310      315      320
Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met Met Phe Pro Gln
      325      330      335
Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe Glu Ser Pro Ile
      340      345      350
Asn Gly Ile Asn Gly
      355

```

<210> 132

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 132

```

Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
 1      5      10      15
Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
      20      25      30
His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
      35      40      45
Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
      50      55      60
Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Leu
65      70      75      80
Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
      85      90      95
Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
      100      105      110
Val Phe Leu Glu Ser Val Asp Leu Ser Ser Asp Trp Asp Ser Gly Ile
      115      120      125
Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
      130      135      140
Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Met Thr Glu Asn
145      150      155      160
His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu
      165      170      175

```



Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala  
                   180                  185                  190  
 Thr Ala Ala Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn  
                   195                  200                  205  
 Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys  
                   210                  215                  220  
 Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val  
 225                  230                  235                  240  
 Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr  
                   245                  250                  255  
 Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg  
                   260                  265                  270  
 Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala  
                   275                  280                  285  
 Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp  
                   290                  295                  300  
 Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met  
 305                  310                  315                  320  
 Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe  
                   325                  330                  335  
 Glu Ser Pro Ile Asn Gly Ile Asn Gly  
                   340                  345

&lt;210&gt; 133

&lt;211&gt; 810

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 133

```

atgacggaga accacacccc ttctaactacg cagccgacgt tgccctgcgcc tgttgctgaa 60
gccgcgccga tccaagcaaa cccggctcct tctgcctcag tcacggcgac tgctgccgcc 120
gctactgcgg cggtgaacaa cgccccctct atgaacggcg ccggtgagca gttgccttgc 180
cagtggggttg gttgcacgga gaagtcccc actgccgagt ctctatatga gcatgtttgc 240
gagcgctcatg ttggacgtaa aagcaccaac aacctcaacc tgacctgcca gtgggggcaact 300
tgcaacacca caacagtcaa gcgtgatcat atcacctccc acatccgcgt tcatgtgcca 360
cttaagccgc acaaatgcga cttttgtggt aaggctttca agcgcccca ggatttgaag 420
aagcatgtca agactcatgc ggacgactcc gagatccgct cccccgaacc gggcatgaag 480
caccctgata tgatgttccc ccaaaacctt aagggttacg ctgctgccac acattacttc 540
gaaagcccta tcaacggcat caatggggga tctaccgcc ccattaccga cgtcagcctg 600
ggggacgagc tccacttaga cggcgaggac gtggcgatgg cgcagccga cgcgctagac 660
gattcgatc tggacatgtt gggggacggg gattccccg gtccgggatt tacccccac 720
gactccgccc cctacggcgc tctggatatg gccgacttcg agtttgagca gatgtttacc 780
gatgccctgg gcattgacga ctttggggga

```

&lt;210&gt; 134

&lt;211&gt; 804

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 134

```

atgacggaga accacacccc ttctaactacg cagccgacgt tgccctgcgcc tgttgetgaa 60
gccgcgccga tccaagcaaa cccggctcct tctgcctcag tcacggcgac tgctgccgcc 120
gctactgcgg cgggtgaacaa cgcctctct atgaacggcg ccggtgagca gttgccttgc 180
cagtgggttg gttgcacgga gaagtcccc actgccgagt ctctatatga gcatgtttgc 240
gagcgtcatg ttggacgtaa aagcaccac aacctcaacc tgacctgcca gtggggcact 300
tgcaacacca caacagtcaa gcgtgatcat atcacctccc acatccgcgt tcatgtgcca 360
cttaagccgc acaaatgcga cttttgtggt aaggctttca agcgcctcca ggatttgaag 420
aagcatgtca agactcatgc ggacgactcc gagatccgct cccccgaacc gggcatgaag 480
caccttgata tgatgttccc ccaaaacct aagggttacg ctgctgccac acattacttc 540
gaaagcccta tcaacggcat caatgggacc gcccccatta ccgacgtcag cctgggggac 600
gagctccact tagacggcga ggacgtggcg atggcgcag ccgacgcgt agacgatttc 660
gatctggaca tgttggggga cggggattcc ccgggtccgg gatttaccac ccacgactcc 720
gccccctacg gcgctctgga tatggcgcac ttcgagtttg agcagatgtt taccgatgcc 780
ctgggcattg acgactttgg ggga 804

```

<210> 135

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 135

```

Met Thr Glu Asn His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala
 1          5          10          15
Pro Val Ala Glu Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala
          20          25          30
Ser Val Thr Ala Thr Ala Ala Ala Thr Ala Ala Val Asn Asn Ala
          35          40          45
Pro Ser Met Asn Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly
          50          55          60
Cys Thr Glu Lys Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys
65          70          75          80
Glu Arg His Val Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys
          85          90          95
Gln Trp Gly Thr Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr
          100          105          110
Ser His Ile Arg Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe
          115          120          125
Cys Gly Lys Ala Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys
          130          135          140
Thr His Ala Asp Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys
145          150          155          160
His Pro Asp Met Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala
          165          170          175
Thr His Tyr Phe Glu Ser Pro Ile Asn Gly Ile Asn Gly Gly Ser Thr
          180          185          190
Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly
          195          200          205
Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu
210          215          220
Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His
225          230          235          240
Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu
          245          250          255
Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly

```

260

265

270

<210> 136  
 <211> 268  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 136  
 Met Thr Glu Asn His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala  
   1                  5                  10                  15  
 Pro Val Ala Glu Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala  
                   20                  25                  30  
 Ser Val Thr Ala Thr Ala Ala Ala Thr Ala Ala Val Asn Asn Ala  
           35                  40                  45  
 Pro Ser Met Asn Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly  
   50                  55                  60  
 Cys Thr Glu Lys Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys  
  65                  70                  75                  80  
 Glu Arg His Val Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys  
                   85                  90                  95  
 Gln Trp Gly Thr Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr  
                  100                 105                 110  
 Ser His Ile Arg Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe  
                  115                 120                 125  
 Cys Gly Lys Ala Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys  
  130                 135                 140  
 Thr His Ala Asp Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys  
  145                 150                 155                 160  
 His Pro Asp Met Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala  
                  165                 170                 175  
 Thr His Tyr Phe Glu Ser Pro Ile Asn Gly Ile Asn Gly Thr Ala Pro  
                  180                 185                 190  
 Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp  
                  195                 200                 205  
 Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met  
  210                 215                 220  
 Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His Asp Ser  
  225                 230                 235                 240  
 Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu Gln Met  
                  245                 250                 255  
 Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly  
                  260                 265

<210> 137  
 <211> 2415  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fungal gene

<400> 137

```

atgggttaaag agagtattat tgctcttgct gagcatgcgg cctccagagc ctcaagagtt 60
attcctccag tgaagctagc ctataaaaat atgcttaagg acccttcctc caagtacaag 120
ccatttaacg ctccaaagct atctaataga aagtggccgg ataaccggat cagcagggct 180
cctcgttggt tatcaacaga tttgagagat ggtaaccaat ctctgccgga tcccatgtca 240
gtggaacaaa agaaagaata ctttcacaag ctgggtcaata ttgggttcaa agaaatcgag 300
gtttccttcc cctctgcata tcaaacagat ttgcacttca ctagatatgc tgtagaaaac 360
gccccagacg atgttagtat tcaatgtctt gtccaatcta gagaacactt gattaagaga 420
acgggtggaag cattaacagg tgctaaaaag gctactatac atacttactt ggcaacaagt 480
gatatgttcc gtgaaattgt ttttaatatg tctagagagg aagctatttc caaggcagta 540
gaggccacca aactagttag gaaactaact aaggatgacc ctcccaaca agccactcgt 600
tggtcctatg agttttcccc cgaatgtttc agtgatactc caggtgaatt tgctgtagaa 660
atttgcgaa gctgttaagaa ggcttgggaa cctaccgagg aaaatccaat cattttcaac 720
ttacctgcta ccgtagaagt tgccctctcca aatgtttatg ctgatcagat tgaatacttc 780
gctacccata ttactgagcg tgagaagggt tgcatctcta cacattgtca caatgaccgt 840
ggttgccgtg tcgccgccac agagttaggt atgcttgca gtgccgaccg tgtagaagga 900
tgtctctttg gtaatggtga acgtacaggt aatgtggact tggttactgt tgctatgaat 960
atgtataccc aagggtgttc tctaatttg gatttctctg acttgacctc tgctctagat 1020
gtggttgagc gttgtaataa gatcccagta tcgcaaagag caccatacgg cggtgacttg 1080
gtcgtttggt ccttttccgg ttctcaccaa gacgccatta agaagggttt caacttaca 1140
aacaagaagc gtgctcaagg tgaaactcaa tggagaatcc catacttgcc attggatcca 1200
aaggacattg gccgtgatta cgaagctgtc atcagagtca actctcagtc tggtaaagg 1260
ggtgccgctt gggttatttt gagatctttg ggtttggatc taccaagaaa catgcaaatc 1320
gaattttcta gcgccgttca agaccatgct gactccttgg gtagagaact aaaatcagat 1380
gagatttcca agttattcaa agaggcttac aactacaatg acgaacagta ccaagctatt 1440
agtttagtca attataatgt tgaaaaatcc ggcaactgac gtagagtgtt cactgggtcaa 1500
gtcaaaagtag gcgaccagat cctctacgcc ggacgcacatc tggccggcat caccggcgcc 1560
acaggtgagg ttgctggcgc ctatatcgcc gacatcaccc atggggaaga tcgggctcgc 1620
cacttcgggc tcatgagcgc ttgtttcggc gtgggtatgg tggcaggccc cgtggccggg 1680
ggactgttgg gcgccatctc cttgcatgca ccattccttg cggcggcggt gctcaacggc 1740
ctcaacctac tactgggctg ctctctaatt caggagtgcg ataaggggaga gcgtcgaccg 1800
atgcccttga gagccttcaa cccagtcagc tccttccggt gggcgcgggg catgactatc 1860
gtcgccgcac ttatgactgt cttctttatc atgcaactcg taggacaggt gccggcagcg 1920
ctctgggtca ttttcggcga ggaccgcttt cgctggagcg cgacgatgat cggcctgtcg 1980
cttcggttat tcggaatctt gcacgccctc gctcaagcct tcgtcactgg tcccgcacc 2040
aaacgtttcg gcgagaagca ggccattatc gccggcatgg cggccgacgc gctgggctac 2100
gtcttgctgg cgttcgcgac gcgaggctgg atggccttcc ccattatgat tcttctcgct 2160
tcggcgggca tcgggatgcc cgcgttgca gccatgctgt ccaggcaggt agatgcagac 2220
catcagggac agcttcaagg atcgctcgcg gctcttacca gcctaacttc gatcactgga 2280
ccgctgatcg tcacggcgat ttatgcgcgc tcggcgagca catggaacgg gttggcatgg 2340
attgtaggcg ccgccctata ccttgtctgc ctccccgcgt tgcgtcgcgg tgcatggagc 2400
cgggccacct cgacc 2415

```

&lt;210&gt; 138

&lt;211&gt; 805

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fungal gene

&lt;400&gt; 138

```

Met Val Lys Glu Ser Ile Ile Ala Leu Ala Glu His Ala Ala Ser Arg
 1             5             10             15
Ala Ser Arg Val Ile Pro Pro Val Lys Leu Ala Tyr Lys Asn Met Leu
 20             25             30
Lys Asp Pro Ser Ser Lys Tyr Lys Pro Phe Asn Ala Pro Lys Leu Ser
 35             40             45

```

Asn	Arg	Lys	Trp	Pro	Asp	Asn	Arg	Ile	Thr	Arg	Ala	Pro	Arg	Trp	Leu	50	55	60
Ser	Thr	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ser	Leu	Pro	Asp	Pro	Met	Ser	65	70	75
Val	Glu	Gln	Lys	Lys	Glu	Tyr	Phe	His	Lys	Leu	Val	Asn	Ile	Gly	Phe	85	90	95
Lys	Glu	Ile	Glu	Val	Ser	Phe	Pro	Ser	Ala	Ser	Gln	Thr	Asp	Phe	Asp	100	105	110
Phe	Thr	Arg	Tyr	Ala	Val	Glu	Asn	Ala	Pro	Asp	Asp	Val	Ser	Ile	Gln	115	120	125
Cys	Leu	Val	Gln	Ser	Arg	Glu	His	Leu	Ile	Lys	Arg	Thr	Val	Glu	Ala	130	135	140
Leu	Thr	Gly	Ala	Lys	Lys	Ala	Thr	Ile	His	Thr	Tyr	Leu	Ala	Thr	Ser	145	150	155
Asp	Met	Phe	Arg	Glu	Ile	Val	Phe	Asn	Met	Ser	Arg	Glu	Glu	Ala	Ile	165	170	175
Ser	Lys	Ala	Val	Glu	Ala	Thr	Lys	Leu	Val	Arg	Lys	Leu	Thr	Lys	Asp	180	185	190
Asp	Pro	Ser	Gln	Gln	Ala	Thr	Arg	Trp	Ser	Tyr	Glu	Phe	Ser	Pro	Glu	195	200	205
Cys	Phe	Ser	Asp	Thr	Pro	Gly	Glu	Phe	Ala	Val	Glu	Ile	Cys	Glu	Ala	210	215	220
Val	Lys	Lys	Ala	Trp	Glu	Pro	Thr	Glu	Glu	Asn	Pro	Ile	Ile	Phe	Asn	225	230	235
Leu	Pro	Ala	Thr	Val	Glu	Val	Ala	Ser	Pro	Asn	Val	Tyr	Ala	Asp	Gln	245	250	255
Ile	Glu	Tyr	Phe	Ala	Thr	His	Ile	Thr	Glu	Arg	Glu	Lys	Val	Cys	Ile	260	265	270
Ser	Thr	His	Cys	His	Asn	Asp	Arg	Gly	Cys	Gly	Val	Ala	Ala	Thr	Glu	275	280	285
Leu	Gly	Met	Leu	Ala	Gly	Ala	Asp	Arg	Val	Glu	Gly	Cys	Leu	Phe	Gly	290	295	300
Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Asp	Leu	Val	Thr	Val	Ala	Met	Asn	305	310	315
Met	Tyr	Thr	Gln	Gly	Val	Ser	Pro	Asn	Leu	Asp	Phe	Ser	Asp	Leu	Thr	325	330	335
Ser	Val	Leu	Asp	Val	Val	Glu	Arg	Cys	Asn	Lys	Ile	Pro	Val	Ser	Gln	340	345	350
Arg	Ala	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Val	Cys	Ala	Phe	Ser	Gly	Ser	355	360	365
His	Gln	Asp	Ala	Ile	Lys	Lys	Gly	Phe	Asn	Leu	Gln	Asn	Lys	Lys	Arg	370	375	380
Ala	Gln	Gly	Glu	Thr	Gln	Trp	Arg	Ile	Pro	Tyr	Leu	Pro	Leu	Asp	Pro	385	390	395
Lys	Asp	Ile	Gly	Arg	Asp	Tyr	Glu	Ala	Val	Ile	Arg	Val	Asn	Ser	Gln	405	410	415
Ser	Gly	Lys	Gly	Gly	Ala	Ala	Trp	Val	Ile	Leu	Arg	Ser	Leu	Gly	Leu	420	425	430
Asp	Leu	Pro	Arg	Asn	Met	Gln	Ile	Glu	Phe	Ser	Ser	Ala	Val	Gln	Asp	435	440	445
His	Ala	Asp	Ser	Leu	Gly	Arg	Glu	Leu	Lys	Ser	Asp	Glu	Ile	Ser	Lys	450	455	460
Leu	Phe	Lys	Glu	Ala	Tyr	Asn	Tyr	Asn	Asp	Glu	Gln	Tyr	Gln	Ala	Ile	465	470	475
Ser	Leu	Val	Asn	Tyr	Asn	Val	Glu	Lys	Phe	Gly	Thr	Glu	Arg	Arg	Val	485	490	495
Phe	Thr	Gly	Gln	Val	Lys	Val	Gly	Asp	Gln	Ile	Leu	Tyr	Ala	Gly	Arg			

[illegible]